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(75) Inventor/Applicant (for US only): BOIVIN, Guy
[CA/CA]; 2531 Montbray, Sainte-Foy, Québec G1V 1E7
(CA).

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(74) Agent: OGILVY RENAULT; Suite 1600, 1981 McGill
College Avenue, Montreal, Québec H3A 2Y3 (CA).

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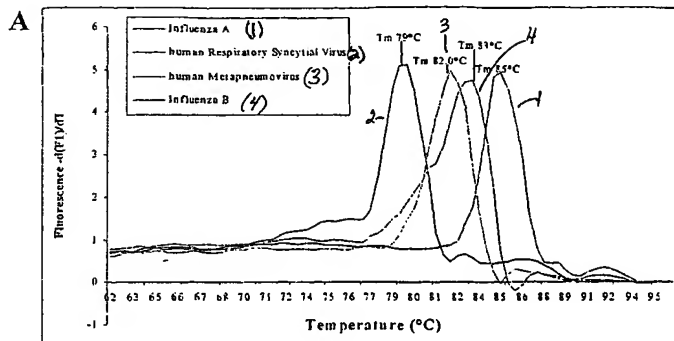
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(71) Applicant (for all designated States except US): UNIVER-
SITÉ LAVAL [CA/CA]; Danielle Allard, Pavillon des sci-
ences de l'éducation, bureau 1474, Québec, Québec G1K
7P4 (CA).

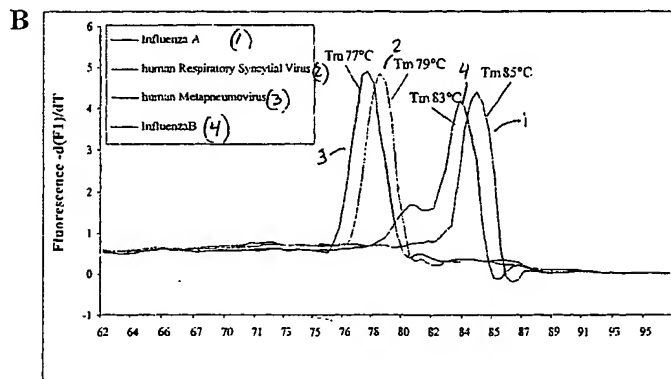
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(54) Title: MOLECULAR METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING RESPIRATORY VIRUSES



(57) Abstract: There is provided compositions and methods for the detection and/or quantification of respiratory viruses using specific nucleic acid sequences. In particular methods and composition are provided to detect human Metapneumovirus (hMPV). The invention also provides with multiplex assays for detecting respiratory viruses in test samples.



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**MOLECULAR METHODS AND COMPOSITIONS FOR DETECTING AND
QUANTIFYING RESPIRATORY VIRUSES**

CROSS-REFERENCE TO RELATED APPLICATIONS

5 This application claims priority on Canadian applications serial number 2,411,264 filed on December 19, 2002 entitled "Sequences for detection and identification of the human metapneumovirus" and serial number 2,418,004 filed on January 24, 2003 entitled "Multiplex assays for detection and identification of viral respiratory pathogens.

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TECHNICAL FIELD

This application relates to the field of microorganisms detection and more particularly to the detection of respiratory tract viruses using virus specific nucleic acids.

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BACKGROUND OF THE INVENTION

Respiratory tract infections are a significant cause of morbidity and mortality in all age groups but especially in young children, elderly subjects, and immunocompromised patients. Most of these infections are caused by viruses with influenza A and B and the human respiratory syncytial virus (hRSV) being associated with the most frequent and severe complications i.e. pneumonitis and death (Dowell et al., 1996, J. Infect. Dis. 174:456-462; Simonsen et al., 2000, J. Infect. Dis. 181:831-837; Han et al., 1999, J. Infect. Dis. 179:25-30; Neuzil et al., 2000, N. Engl. J. Med. 342:225-231; Simoes, 1999, Lancet 354:847-852.). Other viruses such as adenoviruses (> 50 serotypes), parainfluenza viruses (PIV) (4 serotypes), rhinoviruses (> 100 serotypes), and coronaviruses also contribute to acute respiratory tract infections (Trecanor, 2002, Clinical Virology, 2nd ed., ASM Press, Washington, D.C., 7-26). Also, recent studies by the inventor and others have suggested that the new human metapneumovirus (hMPV) should be added to the list of human respiratory viral pathogens in all age groups (van den Hoogen et al., 2001, Nat. Med. 7:719-724;

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Peret et al., 2002, J. Infect. Dis. 185:1660-1663; Boivin et al., 2002, J. Infect. Dis. 186:1330-1334).

The hMPV was initially isolated from nasopharyngeal aspirates recovered from 28 children suffering from respiratory tract infections. Based on partial nucleic acid sequences, gene organization, and electron microscopy (EM) findings, this virus was preliminary assigned to the *Paramyxoviridae* family, subfamily *Pneumovirinae*, genus *Metapneumovirus*. Since then, hMPV has been isolated in North America by our group (Peret et al., 2002, J. Infect. Dis. 185:1660-1663), in Australia (Nissen et al., 2002, Med. J. Aust. 176:188), and in England (Stockton et al., 2002, Emerg. Infect. Dis. 8:897-901).

Preliminary virological characteristics of hMPV.

The initial report by Van Den Hoogen *et al.* (van den Hoogen et al., 2001, Nat. Med. 7:719-724) indicated that the new virus replicated slowly in tertiary monkey kidney (TMK) cells with cytopathic effects (CPE) consisting of syncytium formation appearing 10-14 days post inoculation. Notably, the virus grew very poorly in Vero and A549 cells and could not be propagated in Madin Darby canine kidney (MDCK) cells. Virus-infected TMK cell-culture supernatants also did not display any hemagglutinating activity. The supernatants of infected TMK cells were used for EM studies, which revealed the presence of paramyxovirus-like pleomorphic particles in the range of 150-600 nm with short envelope projections in the range of 13-17 nm. However, RT-PCR studies with primer sets specific for known paramyxoviruses were initially all negative. Using a random PCR amplification procedure known as RAP-PCR (Welsh et al., 1990, Nucleic Acids Res. 18:7213-7218; Ralph et al., 1993, Proc. Natl. Acad. Sci. U.S.A. 90:10710-10714), the Dutch investigators identified differentially displayed bands (compared to human parainfluenza-1 virus) which, upon sequencing, were found to be most closely related to the avian pneumovirus (APV).

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APV, the agent of turkey rhinotracheitis, has been the sole member of the recently assigned *Metapneumovirus* genus within the *Pneumovirinae* subfamily (Taxonomy Virus, 2000, Seventh Report of the International Committee on Taxonomy of Viruses. San Diego. 551, 557, 559-560). The latter virus is a major respiratory pathogen of turkeys and other domestic fowl worldwide (Yu et al., 1992, Virology. 186:426-434; Jones et al., 1987, Vet. Rec. 120:301-302; Jones, 1996, Avian Pathol. 25:639-648; Seal et al., 2000, Virus Res. 66:139-147). There are four serotypes of APV with serotype C (present in US) being the most closely related to hMPV (van den Hoogen et al., 2001, Nat. Med. 7:719-724). The metapneumoviruses (including APV and hMPV) are structurally similar to the human respiratory syncytial virus (hRSV), which also belongs to the *Pneumovirinae* subfamily, except for two features: they lack the two non-structural proteins (NS1 and NS2) and they have a different genomic organization (Yu et al., 1992, Virology. 186:426-434). Recently, an almost complete hMPV sequence (13.4 kb) was reported in GenBank (accession number: AF371337) (van den Hoogen et al., 2002, Virology. 295:119-132). The overall percentage of amino acid sequence identity for the N (nucleoprotein), P (phosphoprotein), M (matrix), F (fusion), M2 (membrane), and L (polymerase) proteins is in the range of 56-88% between hMPV and APV whereas it is 18-44% between hMPV and hRSV. However, the G (glycoprotein) and SH (small hydrophobic) proteins of hMPV do not possess significant amino acid sequence identity with those of any other viruses. In contrast to APV, hMPV was shown to be unable to replicate in turkeys and chickens but the human virus replicated efficiently in the respiratory tract of cynomolgous macaques inducing upper respiratory tract symptoms that correlated with peak viral replication in throat samples between 2 to 8 days post infection (van den Hoogen et al., 2001, Nat. Med. 7:719-724). Thus, these preliminary data indicated that hMPV was a primate pathogen associated with respiratory diseases.

Clinical importance of hMPV.

There is little information about the clinical presentation of hMPV infection. In the original report by Van Den Hoogen *et al.*, 27 of the 28 infected children from the Netherlands were below the age of five (van den Hoogen *et al.*, 2001, *Nat. Med.* 7:719-724). It was mentioned that those infected patients were diagnosed with a range of acute respiratory tract infections (ARTI) from mild to severe including bronchiolitis and pneumonia although no detailed clinical data were provided. In a limited study conducted in the winter of 2000, the same authors found that 7 ($\approx 10\%$) of 68 pediatric patients with unexplained ARTI had evidence of acute hMPV infection by RT-PCR (van den Hoogen *et al.*, 2001, *Nat. Med.* 7:719-724). In addition, Australian investigators reported the detection of hMPV by RT-PCR in 3/200 (1.5%) nasopharyngeal aspirates from children whose specimens were negative for the common respiratory viruses during the winter of 2001 (Nissen *et al.*, 2002, *Med. J. Aust.* 176:188). Recently, hMPV RNA was detected by RT-PCR in 9/405 (2.2%) of nasopharyngeal swabs from English patients who consulted for influenza-like illnesses and had negative tests for other pathogens (Stockton *et al.*, 2002, *Emerg. Infect. Dis.* 8:897-901). These studies, however, suffer from major limitations such as their small size (in most cases), the superficial description of clinical features, the lack of morbidity/mortality data, their retrospective nature, the exclusion of patients who tested positive for other viruses, and the absence of a control group.

Thus far, seroprevalence studies have been limited to the Dutch population. An indirect immunofluorescence assay (IFA) using infected TMK cells has revealed that 25% of the children aged between 6 and 12 months had hMPV antibodies and 70% had become seropositive by the age of 5 years ($n=60$) (van den Hoogen *et al.*, 2001, *Nat. Med.* 7:719-724). Retrospective serological testing also indicates that hMPV has been circulating in the Dutch population for at least half a century.

Diagnosis of hMPV infections

Our laboratory was the first to report the presence of hMPV in America and the second in the world following the initial report from the Netherlands (Peret et al., 2002, *J. Infect. Dis.* 185:1660-1663). Our first 11 hMPV strains were isolated on LLC-MK2 cells, a continuous cell line from rhesus monkey kidneys that is used in our center to recover parainfluenza viruses (PIV). Electron microscopy studies of these isolates revealed pleomorphic, spherical and filamentous particles with characteristics (nucleocapsid diameter and pitch spacing, length of projections) that were consistent with paramyxoviruses. RT-PCR and immunofluorescent assays for paramyxoviruses (PIV 1-3, hRSV) and other respiratory viruses (adenoviruses, coronaviruses, influenza viruses A and B, rhinoviruses) were negative for all 11 isolates. In contrast, amplification of the hMPV F (fusion) and M (matrix) genes based on published partial sequences (van den Hoogen et al., 2001, *Nat. Med.* 7:719-724; van den Hoogen et al., 2002, *Virology*. 295:119-132) was positive for all isolates (Peret et al., 2002, *J. Infect. Dis.* 185:1660-1663).

Subsequently, the virological features and clinical findings associated with a larger set of 38 hMPV strains from subjects hospitalized at our institution (CHUL, Québec City) since 1993 were examined in our laboratory (Boivin et al., 2002, *J. Infect. Dis.* 186:1330-1334). With all cell lines used in our laboratory, we were able to determine that the previously unidentified hMPV strains only consistently grew on LLC-MK2 cells after a mean incubation time of 17.3 days (range 3-23 days). Interestingly, most isolates recovered before 2002 produced only limited syncytia on LLC-MK2 cells, whereas some of the recent strains produced large syncytia typical of those induced by hRSV. Notably, we also observed a seroconversion for hMPV in two adult patients for whom acute and convalescent sera were available using an IFA test designed in our laboratory. Such seroconversion episodes (titers from < 1/10 to 1/80 and from < 1/10 to 1/160 over 2 and 4 weeks, respectively) occurred during the course of the patients' illness suggesting that hMPV was a true respiratory pathogen. A phylogenetic analysis of hMPV Canadian strains based on F gene sequences identified two major phylogenetic groups. At the nucleotide level, we found a similarity of 94.2-100% and 92.6-100% for isolates of groups 1 and 2, respectively, whereas the similarity at the amino acid level was higher i.e. 96.8-100% (group 1) and

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97.2-100% (group 2) suggesting a functional/immunological conservation of the F protein. Interestingly, co-circulation of the two hMPV groups during some years was observed.

5 Over the past 9 years, most (86.7%) hMPV strains from our center were isolated during a 5-month period, from December to May. As an indication of the relative frequency of detection of hMPV compared to other respiratory viruses, we reviewed all respiratory samples (n = 862) sent to our virology laboratory for viral culture during the winter season (Dec. to May) of 2000-01. During this period, hMPV was
10 recovered in 2.3% of all respiratory samples tested by viral culture compared to 2.3% for PIV, 3.4% for adenoviruses, 4.8% for hRSV, and 19.8% for influenza A or B viruses. Overall, hMPV represented 7.1% of all positive cultures from respiratory samples during that winter season with percentages of 4.1%, 2.8%, and 29.3% for
15 patients aged 0-5, 5-65, and > 65 years, respectively. A retrospective review of the clinical charts from hMPV-infected subjects identified for the first time the role of this virus as a cause of severe lower respiratory tract infections in all age groups but especially in young children, elderly subjects, and immunocompromised patients. More specifically, the most frequent diagnoses associated with hMPV infection in hospitalized children were pneumonitis (66%) and bronchiolitis (58.3%) whereas
20 bronchitis/bronchospasm (60%) and pneumonitis (40%) were most commonly seen in elderly subjects (Boivin et al., 2002, J. Infect. Dis. 186:1330-1334). Although no histopathological studies were available, hMPV was the only pathogen identified in respiratory tract secretions of 3 subjects (including 2 with immunosuppressive conditions) who died of respiratory insufficiency.

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We recently studied in greater details one of the cases associated with a fatal hMPV infection (Pelletier et al., 2002, Emerg. Infect. Dis. 8:976-978). Interestingly, this child with acute lymphoblastic leukemia was successively infected by two genetically-distinct hMPV strains on two consecutive winter seasons. On each
30 occasion, hMPV was the only pathogen isolated from a nasopharyngeal aspirate obtained during the course of lower respiratory tract infections (bronchiolitis in the

first year, bronchiolitis followed by fatal pneumonitis in the second year). Comparative sequence analysis of the amplified F gene products (759 bp) revealed that the two viral isolates differed by 114 nucleotides (10 amino acids) and belonged to two different hMPV groups. Overall, our data suggest that many hMPV strains may co-circulate in a specific population during a given period and such viral diversity coupled with a waning immunity (as found in elderly subjects and immunocompromised patients) may lead to multiple and sometimes fatal reinfections similar to those reported with hRSV (Hall, 2001, N. Engl. J. Med. 344:1917-1928; Couch et al., 1997, Am. J. Med. 102:2-9).

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The role and relative contribution of hMPV were recently further expanded in a prospective case-control study performed at our institution during the winter of 2001-02 (Dec. 15-April 20). All children ≤ 3 years were eligible as cases if they were hospitalized for a lower respiratory tract infection (bronchiolitis, croup, pneumonitis) whereas controls consisted of children matched for age and hospitalized for an elective surgery during the same period with no respiratory symptoms. Nasopharyngeal aspirates were obtained from all participants for real-time PCR studies performed on a LightCycler (Roche). The latter included a multiplex RT-PCR for common respiratory viruses (influenza A, influenza B, hRSV) and a real-time RT-PCR assay for hMPV (analytical sensitivity of 100 copies per PCR reaction). No viruses were detected in samples from the 51 control patients. In contrast, at least one virus was identified in samples from 163 (78.4%) of the 208 cases (51% hRSV, 21.6% influenza A, 0% influenza B, 5.8% hMPV, and 5.9% co-infections). hRSV and influenza A infections occurred predominantly in the period between January and March 2002, whereas hMPV infections increased after February. In fact, 11/12 hMPV cases occurred within a 4-week period from mid-March to mid-April accounting for 18.9% of all ARTI in children during this period. Data collected from our virology laboratory indicated that the hMPV outbreak extended after the end of the study protocol (April 20) which suggests that hMPV seasonal pattern may differ from that of other respiratory viruses. A bronchiolitis was diagnosed in 67% of hMPV-infected children whereas 16.7% developed a pneumonia. In brief, there was no statistical

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difference between the different viruses with regard to the symptomatology and reported diagnoses. Similarly, the median duration of hospitalization for the 3 viruses was identical (4-5 days).

- 5 In view of the above, it will be appreciated that diagnosis assay that can rapidly detect the presence of many respiratory viruses is needed.

Respiratory viruses have been classically identified by viral culture using a variety of permissive cell lines. However, viral culture is not convenient for clinical
10 management due to the need of specialized techniques (cell culture, immunofluorescence methods), the long turnaround time before appearance of typical cytopathic effects for many viruses (up to a few weeks), and the need for rapid inoculation of an infectious virus into multiple cell lines for optimal sensitivity (Specter et al., 2002, Clinical Virology, 2nd ed., ASM Press, Washington, D.C., 243-
15 272).

Antigenic detection kits for some respiratory viruses (influenza viruses and hRSV) have been developed by many companies. Most are immunoenzymatic assays (ELISA) based on the capture of a viral antigen by a specific monoclonal antibody.
20 Although such assays eliminate many of the problems inherent to viral cultures (no need for specialized equipment, rapid turnaround time in < 30 min, no need to recover an infectious virus), they have not been widely adopted due to poor sensitivity and/or specificity compared to viral culture. For instance, the sensitivity and specificity of some rapid antigenic tests for influenza has varied from 46 to 96 % and from 52 to 99
25 %, respectively, compared to viral culture. The performance of these tests is dependent on many variables such as the patient's age, the type of specimen and the duration of the disease (Hayden et al., 2002, Clinical Virology, 2nd ed., ASM Press, Washington, D.C., 891-920). The performance of the rapid antigenic tests for hRSV has been considered quite good in children with sensitivity and specificity varying
30 from 80 to 95 % (Piedra et al., 2002, Clinical Virology, 2nd ed., ASM Press, Washington, D.C., 763-790) but poor in adults (Englund et al., 1996, J. Clin.

Microbiol. 34:1649-1653). Detection of antibodies against viral pathogens (serology) has a limited value in the diagnosis of acute viral infections since two serums, collected at a 2 to 3 week interval, are required in order to document a significant rise in viral antibody titers.

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More recently, PCR or RT-PCR assays have been developed for many respiratory viruses allowing detection of small amounts of viral DNA or RNA in a clinical sample. In the so-called "multiplex" format, PCR assays have been designed to amplify more than one viral target in the same PCR reaction (Ellis et al., 1997, J. Clin. Microbiol. 35:2076-2082; Fan et al., 1998, Clin. Infect. Dis. 26:1397-1402; Liolios et al., 2001, J. Clin. Microbiol. 39:2779-2783; Grondahl et al., 1999, J. Clin. Microbiol. 37:1-7). However, most multiplex PCR assays reported to date do not allow the simultaneous detection of all viruses involved in acute respiratory tract infections of humans and they require separate steps for the amplification and detection of viral genes, greatly increasing the assay's turnaround time and preventing reliable quantification of the amplicons. At present, only one multiplex PCR assay (the Hexaplex test from Prodesse, Waukesha, WI) is commercially-available. The Hexaplex detects 6 respiratory viruses (influenza A and B, PIV 1-3 and hRSV) using specific viral probes in a microplate format (Fan et al., 1998, Clin. Infect. Dis. 26:1397-1402; Kehl et al., 2001, J. Clin. Microbiol. 39:1696-1701). This assay does not use real-time amplification methodologies and has a turnaround time of about one full working day. Thus, there is a need for developing more rapid molecular assays that permit detection of a larger panel of respiratory viral pathogens.

25 Rapid and sensitive detection of respiratory viruses is an important clinical goal to help physicians select the most appropriate antiviral, reduce nosocomial transmission of pathogens, decrease the length of hospitalization, and reduce antibiotic use and bacterial resistance. The present invention relates to the development of multiplex assays based on nucleic acids detection for sensitive and rapid diagnosis of most viral
30 respiratory pathogens of humans.

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SUMMARY OF THE INVENTION

It is an object of the present invention to provide a rapid and sensitive method using amplification primers and/or probes for determining the presence and/or the amount in a test sample of nucleic acids from clinically important respiratory viral pathogens including human metapneumovirus.

In another aspect there is provided multiplex assays aimed at detecting conserved genes of common respiratory viral pathogens such as influenza A and B, human respiratory syncytial virus (hRSV) A and B, human metapneumovirus (hMPV), parainfluenza viruses (PIV) types 1-4, adenoviruses, rhinoviruses, enteroviruses, and coronaviruses.

The nucleic acid amplification method is preferably but not exclusively PCR. In a preferred embodiment, identification of the amplicons produced by the amplification of nucleic acids from respiratory viruses is achieved by verifying the specific melting temperature of amplified viral products or by hybridization with specific viral probes. Other amplification technologies including target and probe amplification techniques as well as signal amplification techniques performed in liquid phase or onto solid supports may also be used.

It is an object of the present invention to provide a method using nucleic acid amplification and/or detection for determining the presence and/or the amount of nucleic acids of the human metapneumovirus (hMPV).

In a preferred embodiment, the nucleic acid amplification method is PCR. However, other amplification technologies including target and probe amplification techniques as well as signal amplification performed in liquid phase or onto solid support may also be used.

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This invention provides a method to detect the presence of hMPV in a test sample based on the detection of a nucleotide sequence from either the nucleocapsid (N), phosphoprotein (P), matrix (M), fusion (F), membrane (M2), polymerase (L), glycoprotein (G), and small hydrophobic (SH) genes. In a particularly preferred embodiment, the method to detect the presence of hMPV in a test sample is based on the detection of a nucleotide sequence from the nucleoprotein (N) or polymerase (L) genes.

In another embodiment, identification of amplified hMPV products is achieved by verifying the specific melting temperature of amplified viral products or by hybridization with hMPV-specific probes.

It is another object of this invention to provide a method for typing hMPV strains which comprises the steps of reproducing the above amplification method followed by either hybridization using type-specific probes, DNA sequencing or restriction enzyme analysis. Typing is done preferentially, but not exclusively, on the most variable hMPV genes i.e. the fusion (F) and glycoprotein (G) genes.

All the proprietary DNA fragments and oligonucleolides useful in the detection or identification of a hMPV strain are further objects of this invention as well as any composition of matters that include them (recombinant vectors, hosts, diagnostic kits...).

BRIEF DESCRIPTION OF THE DRAWINGS

Further features and advantages of the present invention will become apparent from the following detailed description, taken in combination with the appended drawings, in which:

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Figure 1 represents a melting curve analysis of amplified hMPV strains using specific nucleoprotein primers (Sequence ID Nos. 92 and 94) ;

Figure 2 shows an ethidium bromide-stained agarose gel showing restriction fragment
5 length polymorphism of amplified hMPV fusion (F) gene sequences digested with
enzymes ApaI and Avr II. PCR products of the hMPV F gene (amplified with
primers sequence ID Nos. 97 and 98) were digested with ApaI and Avr II. Strains
belonging to hMPV genotype F-1 were digested only by ApaI resulting in two
fragments of 532 bp and 227 bp whereas strains belonging to hMPV genotype F-2
10 were digested only by Avr II resulting in fragments of 447 and 312 bp.;

Figure 3 shows the age at admission of children hospitalized for acute respiratory tract
infections (ARTI) caused by hMPV (A), hRSV (B), and influenza A (C) as well as for
the whole study population (D) described in example 4;

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Figure 4 represents the biweekly distribution of virologically cases with acute
respiratory tract infections and their controls in the study reported in example 4;

Figure 5 represents the biweekly distribution of hMPV isolates in the study group
20 (hospitalized children) described in example 4 and in respiratory specimens tested at
the regional virology laboratory (RVL);

Figure 6 illustrates a phylogenetic tree of hMPV strains recovered as part of the study
described in example 4 also including the prototype strain from the Netherlands
25 (GenBank af371367) and a Canadian isolate from season 2000-01 (hMPV35-2001).
The dates of sample collection are in parentheses;

Figure 7 is a melting curve analysis of viral strains amplified using the respiratory-1
multiplex real-time PCR assay. A- Multiplex real-time PCR assay using hMPV N
30 primers (SEQ ID NOS. 95 and 96). B- Multiplex real-time PCR assay using hMPV L

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primers (SEQ ID NOS. 112 and 114). Note: the internal control is apparent (T_m: 91°C) in the absence of amplification of specific viral products;

5 Figure 8 is a melting curve analysis of viral strains amplified using the respiratory-2 multiplex real-time PCR assay. Note: The internal control is apparent (T_m: 91°C) in the absence of amplification of specific viral products;

10 Figure 9A is a fluorescence signal as a function of elongation step for the determination of the hMPV load in clinical samples using quantitative real-time PCR;

Figure 9B is a standard curve for determination of the hMPV using quantitative real-time PCR;

15 Figure 10A is a phylogenetic tree for the F gene of hMPV;

Figure 10B is a phylogenetic tree for the G gene of hMPV;

20 Figure 11 is a melting curve analysis of amplified viral genes and of an internal control as determined by the LightCycler instrument. Note that high amounts of amplified viral products may preclude detection of the internal control in some PCR runs; and

Figure 12 is a melting curve analysis SARS-coronavirus using a real time PCR assay.

25 It will be noted that throughout the appended drawings, like features are identified by like reference numerals.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

The invention provides nucleic acid based diagnostic methods and compositions to detect and quantify respiratory viruses.

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In a preferred embodiment respiratory viral pathogens targeted by the diagnostic assays include all genotypes of influenza A and B viruses, hRSV, hMPV, PIV, adenoviruses, rhinoviruses, and enteroviruses. Other less common (coronaviruses, reoviruses) and yet to be discovered respiratory viruses are also targets under the scope of the present invention.

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In the description of this invention, the terms «nucleic acids» and «sequences» might be used interchangeably. However, «nucleic acids» are chemical entities while «sequences» are the pieces of information encoded by these «nucleic acids». Both nucleic acids and sequences are equivalently valuable sources of information for the matter pertaining to this invention.

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In one embodiment the method targets conserved hMPV nucleotide sequences for diagnostic purposes and variable hMPV sequences for epidemiological typing purposes. Nucleotide sequences were selected either from a number of hMPV viral sequences obtained in the inventor's laboratory or from public databases (GenBank accession number AF371337).

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Our proprietary DNA fragments and oligonucleotides (a non-restrictive list of primers and probes) are listed in the following tables.

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It will be understood by those skilled in the art that sequences that can selectively hybridize to the sequences of the present invention are also comprised in the scope of the invention. By selectively hybridizing it is meant that a nucleic acid molecule binds to a given target in a manner that is detectable in a different manner from non-target

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sequence under moderate, or more preferably under high, stringency conditions of *hybridization*. "Complementary" or "target" nucleic acid sequences refer to those nucleic acid sequences which selectively hybridize to a nucleic acid molecule. Proper annealing conditions depend, for example, upon a nucleic acid molecule's length, base composition, and the number of mismatches and their position on the molecule, and must often be determined empirically. For discussions of nucleic acid molecule (probe) design and annealing conditions, see, for example, Sambrook et al. 1989 (Sambrook, et al., *Molecular Cloning: A Laboratory Manual*, 2d Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)) or Ausubel et al. 1987 (Ausubel, F., et al., *Current Protocols in Molecular Biology*, New York (1987)).

The detection of the viruses including the hMPV is conducted through compositions of matters such as diagnostic kits comprising the amplification primers or probes of this invention.

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In the methods and kits of the present invention, probes and primers are not limited to nucleic acids and may include, but are not restricted to, analogs of nucleotides. The diagnostic reagents constituted by the probes and the primers may be present in any suitable form (bound to a solid support, liquid, lyophilized, etc.) for detection and/or amplification of nucleic acid sequences of the viruses.

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In the methods and kits of the present invention, amplification reactions may include but are not restricted to: a) polymerase chain reaction (PCR), b) ligase chain reaction (LCR), c) nucleic acid sequence-based amplification (NASBA), d) self-sustained sequence replication (3SR), e) strand displacement amplification (SDA), f) branched DNA signal amplification (bDNA), g) transcription-mediated amplification (TMA), h) cycling probe technology (CPT), i) nested PCR, j) multiplex PCR, k) solid phase amplification (SPA), l) nuclease dependent signal amplification (NDSA), m) rolling circle amplification technology (RCA), n) anchored strand displacement amplification, o) solid-phase (immobilized) rolling circle amplification.

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In the methods and kits of the present invention, detection of the nucleic acids of target genes may include real-time or post-amplification technologies. These detection technologies can include, but are not limited to, the use of intercalating agents such as SYBR green, fluorescence resonance energy transfer (FRET)-based methods such as adjacent hybridization of probes (including probe-probe and probe-primer methods), *TaqMan* probe, molecular beacon probe, Scorpion probe, nanoparticle probe and Amplifluor probe. Other detection methods include target gene nucleic acids detection via immunological methods, solid phase hybridization methods on filters, chips or any other solid support. In these systems, the hybridization can be monitored by fluorescence, chemiluminescence, potentiometry, mass spectrometry, plasmon resonance, polarimetry, colorimetry, flow cytometry or scanometry. Nucleotide sequencing, including sequencing by dideoxy termination or sequencing by hybridization (e.g. sequencing using a DNA chip) represents another method to detect and characterize the nucleic acids of target genes.

Amplification of hMPV sequences

In one aspect of the invention there is provided methods and compositions for detecting hMPV in a sample.

In a preferred embodiment, a reverse-transcription (RT)-PCR protocol is used for nucleic acid amplification. The single-stranded viral RNA is converted to complementary DNA using an enzyme possessing a reverse transcriptase activity and a specific hMPV primer. Alternatively, random hexamer primers can be substituted to the specific hMPV primer. In a preferred embodiment, viral RNA was prealably extracted from 200 μ l of naso-pharyngeal aspirates using the QIAamp Viral RNA Mini Kit (QIAGEN). Complementary DNA was synthesized using 10 μ l of eluted RNA, 0.75 μ M of a specific hMPV primer (Table 2, sequences ID Nos. 91, 97, 100, 102, 109, 112), and the Omniscript Reverse Transcriptase Kit (QIAGEN, Mississauga, ON, Canada) following the manufacturer's recommendations.

- For DNA amplification by the widely used PCR method, primer pairs were derived from our proprietary DNA fragments or from public database sequences (Table 1). During DNA amplification by PCR, two oligonucleotide primers binding respectively to each strand of the heat-denatured target DNA from the microbial genome are used
- 5 to amplify exponentially *in vitro* the target DNA by successive thermal cycles allowing denaturation of the DNA, annealing of the primers and synthesis of new targets at each cycle (Persing, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, DC. 88-109).
- 10 In a preferred embodiment, complementary DNA was amplified using a real-time PCR procedure with the LC Faststart DNA Master SYBR Green 1 Kit (Roche Diagnostics, Laval, QC, Canada) or the SYBR Green TAQ ReadyMix for quantitative PCR capillary formulation (Sigma-Aldrich, Oakville, ON) in a LightCycler instrument (Roche Diagnostics). Each reaction had a total volume of 20 μ l including 2
- 15 μ l of RT mixture and 18 μ l of a reaction mixture containing 4 mM $MgCl_2$, 2 μ l of Faststart DNA SYBR Green Master Mix or the SYBR Green TAQ ReadyMix for quantitative PCR capillary formulation, 3% DMSO, and 0.5 μ M of each hMPV primer (see Tables 2 and 4 for sequence ID Nos. and specific combinations of primers for amplification, respectively). Cycling conditions typically included an initial
- 20 denaturation step of 10 min. at 94°C, followed by 50 cycles of 15 s at 94°C, 5 s at 54°C, and 30 s at 72°C. However, the cycling conditions could slightly vary according to the hMPV gene to amplify.
- The person skilled in the art of nucleic acid and/or signal amplification knows the
- 25 existence of other rapid amplification procedures such as ligase chain reaction (LCR), reverse transcriptase PCR (RT-PCR), transcription-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA), branched DNA (bdNA), cycling probe technology (CPT), solid phase amplification (SPA), rolling circle
- 30 amplification technology (RCA), solid phase RCA, anchored SDA and nuclease dependent signal amplification (NDSA) (Persing, 1993, Diagnostic Molecular

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Microbiology: Principles and Applications, American Society for Microbiology, Washington, DC. 88-109; Lee, 1997, Nucleic Acid Amplification Technologies: Applications to Disease Diagnosis, Eaton Publishing, Boston, MA. 61-125; Westin et al., 2000, Nat. Biotechnol. 18:199-204). The scope of this invention is not limited to the use of amplification by PCR, but rather includes the use of any nucleic acid amplification method or any other procedure which may be used to increase the sensitivity and/or the rapidity of nucleic acid-based diagnostic tests. The scope of the present invention also covers the use of any nucleic acid and/or signal amplification and detection technology including real-time or post-amplification detection technologies, any amplification technology combined with detection, any hybridization nucleic acid chips or array technologies, any amplification chips or combination of amplification and hybridization chip technologies. Detection and identification by any nucleotide sequencing method is also under the scope of the present invention.

Any oligonucleotide, useful for diagnosis, and which are derived from hMPV sequences and used with any nucleic acid amplification and/or hybridization technologies are also under the scope of this invention.

Detection of amplification products

Classically, the detection of PCR amplification products is performed by standard ethidium bromide-stained agarose gel electrophoresis. Using this approach, primers specific for a nucleotide sequence from either the nucleocapsid (N), phosphoprotein (P), matrix (M), fusion (F), polymerase (L), glycoprotein (G), genes generated amplicons of various lengths depending on the selected primers pairs (Table 4). It is however clear that other detection methods of amplified products may be faster, more sensitive, and more practical. Amplicon detection may also be performed by solid support or liquid hybridization using strain-specific internal DNA probes hybridizing to an amplification product. Such probes may be generated from sequences from our repertory (Table 1) and designed to specifically hybridize to DNA amplification

products which are objects of the present invention. Amplicons can also be characterized by DNA sequencing. Alternatively, a rapid detection method developed with real-time PCR assays consists of determining the specific melting temperature of amplicons at the end of the amplification reaction.

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In a preferred embodiment, detection of hMPV amplicons was characterized using the melting curve analysis feature of a real-time PCR instrument. Briefly, following the last amplification cycle on a LightCycler instrument, the internal temperature was rapidly increased to 94°C then decreased to 60°C for 30 seconds, followed by slowly increasing to 94°C at a rate of 0.1°C per second, with continuous fluorescence lecture. Using this procedure, the specific melting temperature obtained with the specific amplicons produced by the pairs of primers specific for the N (SEQ ID No 92+94), M (SEQ ID No 100+101), F (SEQ ID 97+98), P (SEQ ID No 102 +103) and L (SEQ ID No 112 + 113) gene sequences was found to be 82.63°C \pm 0.87°C, 82.75°C \pm 0.80°C, 83.29°C \pm 0.45°C, 80.48°C \pm 0.46°C, and 77.99 \pm 0.33°C, respectively (Table 5 and see also Figure 1 for example of the melting temperature obtained for different hMPV strains with the N primers). Alternatively, we also designed specific adjacent and TaqMan fluorescent probes for the various hMPV gene products (N, M, F, G, P and L) that can be used for real-time detection and quantification of amplicons (Table 3). Here, quantification of hMPV gene products is achieved through fluorescence resonance energy transfer (FRET) when the two probes hybridize nearby on a complementary DNA sequence. Other types of detection methods including the use of TaqMan or molecular beacon probes specific for the hMPV sequences described above are also under the scope of this invention.

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Typing of hMPV

Previous studies have shown that two major genotypes of hMPV circulate in North America and Europe (van den Hoogen et al., 2001, Nat. Med. 7:719-724; Boivin et al., 2002, J. Infect. Dis. 186:1330-1334). We also designed a rapid molecular typing method for epidemiologic studies based on amplification of a portion of the F (fusion)

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glycoprotein (primer sequence ID Nos. 97 and 98, Tables 2 and 4) followed by DNA sequencing or digestion with restriction enzymes (ApaI I and Avr II). Table 6 summarizes the size of the F fragments obtained for different hMPV isolates following enzymatic digestion and the corresponding genotype (see also Figure 2 for an example of the band pattern following electrophoresis on an agarose gel). Alternative typing methods based on the use of type-specific hMPV F primers and/or probes as well as DNA sequencing of amplified products are also within the scope of this invention. hMPV subtyping using similar methodologies for the other surface glycoprotein (i.e. the G gene) may also be used.

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A method for detection of a plurality of potential hMPV strains having different genotypes may be conducted in separate reactions and physical enclosures, one type at the time. Alternatively, it could be conducted simultaneously for different types in separate physical enclosures, or in the same physical enclosures. In the latter scenario a multiplex PCR reaction could be conducted which would require that the oligonucleotides are all capable of annealing with a target region under common conditions. Since many probes or primers are specific for a determined genotype, typing an hMPV strain is under the scope of the present invention. When a mixture of oligonucleotides annealing together with more than one type of hMPV is used in a single physical enclosure or container, different detection labels would be used to distinguish one type from another.

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The diagnostic kits, primers and/or probes mentioned above can be used to detect and/or identify hMPV, whether said diagnostic kits, primers and probes are used for *in vitro* or *in situ* applications. The said samples may include but are not limited to: any clinical sample, any environmental sample, any viral culture, any tissue, or any cell line.

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It is also an object of the present invention that said diagnostic kits, primers and/or probes can be used alone or in combination with any other assay suitable to detect and/or identify other microorganisms (i.e. viruses, bacteria, fungi, and parasites) including but not limited to: any assay based on nucleic acids detection, any

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immunoassay, any enzymatic assay, any biochemical assay, any lysotypic assay, any serological assay, any culture on specific cell lines, and any infectivity assay on animals.

- 5 In the methods and kits described herein below, the oligonucleotide probes and amplification primers have been derived from larger sequences (i.e. DNA fragments of at least 100 base pairs). All DNA sequences have been obtained either from our proprietary sequences (Table 1) or from SEQ ID No. 1 from public databases.
- 10 It is clear to the individual skilled in the art that oligonucleotide sequences other than those described in the present invention and which are appropriate for detection and/or identification of hMPV may also be derived from the proprietary fragment sequences or selected public database sequences. For example, the oligonucleotide primers or probes may be shorter but of a length of at least 10 nucleotides or longer
- 15 than the ones chosen; they may also be selected anywhere else in the proprietary DNA fragments or in the sequences selected from public databases; they may also be variants of the same oligonucleotide. If the target DNA or a variant thereof hybridizes to a given oligonucleotide, or if the target DNA or a variant thereof can be amplified by a given oligonucleotide PCR primer pair, the converse is also true : a given target
- 20 DNA may hybridize to a variant oligonucleotide probe or be amplified by a variant oligonucleotide PCR primer. Alternatively, the oligonucleotides may be designed from said DNA fragment sequences for use in amplification methods other than PCR. Consequently, the core of this invention is the detection and/or identification of hMPV by targeting DNA sequences which are used as a source of specific and
- 25 ubiquitous oligonucleotide probes and/or amplification primers. Although the selection and evaluation of oligonucleotides suitable for diagnostic purposes require much effort, it is quite possible for the individual skilled in the art to derive, from the selected DNA fragments, oligonucleotides other than the ones listed in Tables 2 and 3 which are suitable for diagnostic purposes. When a proprietary fragment or a public
- 30 database sequence is selected for its specificity and ubiquity (i.e. ability to detect all

hMPV strains), it increases the probability that subsets thereof will also be specific and ubiquitous.

The proprietary DNA fragments have been obtained as a repertory of sequences created by amplifying hMPV nucleic acids with proprietary primers. These primers and the repertory of nucleic acids as well as the repertory of nucleotide sequences are further objects of this invention (Tables 1-3).

As part of the design rules, all oligonucleotides were evaluated for their suitability for hybridization or PCR amplification by computer analysis using standard programs (i.e. the GCG Wisconsin package programs, the primer analysis software Oligo™ 6 and MFOLD 3.0). The potential suitability of the PCR primer pairs was also evaluated prior to their synthesis by verifying the absence of unwanted features such as long stretches of the same nucleotide and a high proportion of G or C residues at the 3' end (Persing, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, DC. 88-109). Oligonucleotide amplification primers were synthesized using an automated DNA synthesizer (Applied Biosystems).

The oligonucleotide sequence of primers or probes may be derived from either strand of the duplex DNA. The primers or probes may consist of the bases A, G, C, or T or analogs and they may be degenerated at one or more chosen nucleotide position(s) (Nichols et al., 1994, Nature. 369:492-493). Primers and probes may also consist of nucleotide analogs such as Locked Nucleic Acids (LNA) (Koskhin et al., 1998, Tetrahedron Lett. 54:3607-3630), and Peptide Nucleic Acids (PNA) (Egholm et al., 1993, Nature. 365:566-568). The primers or probes may be of any suitable length and may be selected anywhere within the DNA sequences from proprietary fragments, or from selected database sequences which are suitable for the detection of hMPV.

Variants for a given target microbial gene are naturally occurring and are attributable to sequence variation within that gene. For example, different strains of the same viral

species may have a single or more nucleotide variation(s) at the oligonucleotide hybridization site. The person skilled in the art is well aware of the existence of variant nucleic acids and/or sequences for a specific gene and that the frequency of sequence variations depends on the selective pressure during evolution on a given gene product. The detection of a variant sequence for a region between two PCR primers may be demonstrated by sequencing the amplification product. In order to show the presence of sequence variations at the primer hybridization site, one has to amplify a larger DNA target with PCR primers outside that hybridization site. Sequencing of this larger fragment will allow the detection of sequence variation at this primer hybridization site. A similar strategy may be applied to show variations at the hybridization site of a probe. Insofar as the divergence of the target nucleic acids and/or sequences or a part thereof does not affect significantly the sensitivity and/or specificity and/or ubiquity of the amplification primers or probes, variant microbial DNA is under the scope of this invention. Variants of the selected primers or probes may also be used to amplify or hybridize to a variant target DNA.

In an other aspect of the invention there is also provided newly isolated human metapneumoviruses deposited with International Depository Authority of Canada on December 11 2003 and bearing IDAC numbers 111203-01 and 111203-02 (also referred herein as CAN 97-83 and CAN 98-75 respectively).

In a further aspect of the invention the diagnostic method is designed at performing simultaneous detection of nucleic acids from a variety of respiratory viruses using specific primers and/or probes. The method is aimed at detecting and/or quantifying conserved viral sequences from respiratory viruses for diagnostic purposes. Target nucleotide sequences were selected public databases and from viral strain sequences obtained in the inventor's laboratory.

The specific respiratory viral pathogens targeted by the diagnostic assays include all genotypes of influenza A and B viruses, hRSV, hMPV, PIV, adenoviruses, rhinoviruses, and enteroviruses. Other less common (coronaviruses, reoviruses) and

yet to discover respiratory viruses are also targets under the scope of the present invention.

The specific combination of oligonucleotides (primers and/or probes) in a multiplex
5 format is also another object of this invention.

Composition of matters such as diagnostic kits comprising amplification primers and/or probes for the detection of respiratory viruses are also objects of the present invention.

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Amplification of viral sequences

In a preferred embodiment, a PCR protocol is used for nucleic acid amplification. Multiplex assay, aimed at amplifying a plurality of respiratory viruses in the same
15 physical enclosure, is an object of the present invention.

We aim at developing DNA-based tests or diagnostic kits to detect and identify most respiratory viruses in a limited number of amplification reactions using specific primers (Table 10) and/or probes (Table 11). Although some of the primer sequences
20 used for amplification of the various respiratory viruses, with the exception of hMPV (SEQ. ID. Nos. 95 and 96 or 112 and 114), PIV-1 (SEQ. ID. Nos. 147 and 148), PIV-3 (SEQ. ID. Nos. 151 and 152), and adenovirus (SEQ. ID. Nos. 153), have been described previously by others (Fouchier et al., 2000, J. Clin. Microbiol. 38:4096-4101 for influenza A virus / SEQ. ID. Nos. 139 and 140; Li et al., 2001, J. Clin.
25 Microbiol. 39:696-704 for influenza B virus / SEQ. ID. Nos. 141 and 142; Mazulli et al., 1999, J. Infect. Dis. 180:1686-1689 for hRSV / SEQ. ID. Nos. 143 and 144; Osiowy et al., 1998, J. Clin. Microbiol. 36: 3149-3154 for PIV-1, PIV-3, and adenovirus / SEQ. ID. Nos. 145 and 146, 149 and 150, and 154 and 155, respectively; Amar et al., 1993, J. Clin. Microbiol. 31: 2544-2546 for rhinovirus and enterovirus /
30 SEQ. ID. Nos. 160 and 161) and that one influenza A primer (SEQ. ID. No. 139) is

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almost identical to the one described in another patent (U.S. patent number 6,015,664), the object of the present invention is to combine many sets of primers and/or probes in the same physical enclosure (multiplex format).

- 5 Briefly, viral RNA was extracted from 200 μ l of naso-pharyngeal aspirates or other respiratory tract samples using the QIAamp Viral RNA Mini kit (QIAGEN, Mississauga, ON, Canada). Complementary DNA (cDNA) was then synthesized using 10 μ l of the RNA preparation, 0.75 μ M of random hexamer primers (Amersham Pharmacia Biotech, Baie d'Urfé, QC, Canada), 300 copies of an internal control
10 template, and the Omniscript Reverse Transcriptase Kit (QIAGEN, Mississauga, ON, Canada) following the manufacturer's instructions. The internal control template consisted of a 554 or 558 bp (depending on the multiplex assay) transcribed region of an herpes simplex virus type 2 DNA polymerase region flanked by either influenza B or rhinovirus/enterovirus complementary primer sequences (depending on the
15 multiplex assay) cloned in the pDrive plasmid (QIAGEN).

- For DNA amplification by the widely used PCR method, primer pairs were mostly derived from public database sequences (Table 10). During DNA amplification by PCR, two oligonucleotide primers binding respectively to each strand of the heat-
20 denatured target DNA from the viral genome are used to amplify exponentially *in vitro* the target DNA by successive thermal cycles allowing denaturation of the DNA, annealing of the primers and synthesis of new targets at each cycle (Persing, 1993, Diagnosis Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C., 88-109).

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- In a preferred embodiment, cDNA was amplified using a real-time PCR procedure with the LC Faststart DNA Master SYBR Green 1 Kit (Roche Diagnostics, Laval, QC, Canada) or the SYBR Green TAQ ReadyMix for quantitative PCR capillary formulation (Sigma-Aldrich, Oakville, ON) in a LightCycler instrument (Roche
30 Diagnostics). Each reaction had a total volume of 20 μ l including 2 μ l of cDNA and 18 μ l of a reaction mixture containing 4 mM $MgCl_2$, 2 μ l of LC Faststart DNA SYBR

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Green 1 Master Mix or the SYBR Green TAQ ReadyMix for quantitative PCR capillary formulation, 3% DMSO, and 0.3-1.0 μ M of each viral primer (see Tables 10, 12, and 13 for primer sequence ID NOs., length of amplicons, and specific combination of primers, respectively). Cycling conditions typically included an initial
5 denaturation step of 10 min at 94°C, followed by 50 cycles of 15 s at 94°C, 5 s at 58°C, and 25 s at 72°C. However, the cycling conditions could vary slightly according to the multiplex PCR assay.

In a preferred embodiment, two real-time multiplex PCR assays were used to amplify
10 and detect the panel of common respiratory viruses (Table 13). The respiratory-1 multiplex assay combines 4 sets of primers for amplification of influenza A and B viruses, hRSV, hMPV, and an internal control template. The respiratory-2 multiplex assay comprises 4 other sets of primers for amplification of PIV-1, PIV-3, adenoviruses, rhinoviruses/enteroviruses, and an internal control template. The use of
15 any other combinations of the same or similar primer sequences in two or more than two multiplex assays for detection of common respiratory viral pathogens is also under the scope of this invention.

The person skilled in the art of nucleic acid amplification knows the existence of other
20 rapid amplification procedures such as ligase chain reaction (LCR), reverse transcriptase PCR (RT-PCR), solid phase PCR, transcription-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA), branched DNA (bDNA), cycling probe technology (CPT), solid phase amplification (SPA), rolling
25 circle amplification technology (RCA), solid phase RCA, anchored SDA, and nuclease dependent signal amplification (NDSA) (Persing, 1993, Diagnosis Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C., 88-109; Lee, 1997, Nucleic Acid Amplification Technologies: Application to Disease Diagnosis, Eaton Publishing, Boston, MA., 61-125; Westin et
30 al., 2000, Nat. Biotechnol.18:199-204). The scope of this invention is not limited to the use of amplification by PCR, but rather includes the use of any nucleic acid

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amplification method or any other procedure which may be used to increase the sensitivity and/or the rapidity of nucleic acid-based diagnostic tests. The scope of the present invention also covers the use of any nucleic acids amplification and detection technology including real-time or post-amplification detection technologies, any amplification technology combined with detection, any hybridization nucleic acid chips or array technologies, any amplification chips or combination of amplification and hybridization chip technologies. Detection and identification by any nucleotide sequencing method is also under the scope of the present invention.

10 Detection of amplification products

Classically, the detection of PCR amplification products is performed by standard ethidium bromide-stained agarose gel electrophoresis. Using this approach, the amplicons may be discriminated based on their size. In the present invention, the length of the different amplicons varies from 84 to 929 bp (Table 12). It is however clear that other detection methods of amplified products may be faster, more sensitive, and more practical. Amplicon detection may also be performed by solid support or liquid hybridization using strain-specific, internal DNA probes hybridizing to an amplification product. Such probes may be generated from sequences designed to specifically hybridize to DNA amplification products which are objects of the present invention. Amplicons can be also characterized by DNA sequencing. Alternatively, a rapid detection method developed with real-time PCR assays consist of determining the specific melting temperature of amplicons at the end of the amplification reaction.

The detection of viral amplicons was first characterized using the melting curve analysis feature of a real-time PCR instrument. Using this procedure, the different viral targets amplified in each of the multiplex PCR assays could be differentiated by their specific melting temperature (Table 13 and Fig. 7 and 8). Alternatively, specific fluorescent probes (Table 11) for each viral target can be used for real-time detection and quantification of amplicons in a single amplification/detection assay. Real-time quantification of viral products can be performed through a variety of fluorescence-

based technologies such as adjacent probes, Taqman probes, and molecular beacons. Alternatively, these probes may be used in a separate post-amplification step.

The diagnostic kits, primers and probes mentioned above can be used to detect and/or
5 identify respiratory viruses, whether said diagnostic kits, primers and/or probes are used for *in vitro* or *in situ* applications. The said samples may include but are not limited to: any clinical sample, any environmental sample, any viral culture, any tissue, and any cell line.

10 It is also an object of the present invention that said diagnostic kits, primers and/or probes can be used alone or in combination with any other assay suitable to detect and/or identify and/or quantify microorganisms, including but not limited to: any assay based on nucleic acids detection, any immunoassay, any enzymatic assay, any biochemical assay, any serological assay, any culture on specific cell lines, and any
15 infectivity assay on animals.

In the methods and kits described herein, the oligonucleotide probes and amplification primers have been derived from larger sequences (i.e. DNA fragments of at least 100 base pairs). It is clear to the individual skilled in the art that oligonucleotide sequences
20 other than those described in the present invention and which are appropriate for detection and/or identification of any respiratory viruses may also be derived from those selected in the present invention. For example, the oligonucleotide primers or probes may be shorter but of a length of at least 10 nucleotides or longer than the ones chosen; they may also be variants of the same oligonucleotide. If the target DNA or a
25 variant thereof hybridizes to a given oligonucleotide, or if the target DNA or a variant thereof can be amplified by a given oligonucleotide PCR primer pair, the converse is also true; a given target DNA may hybridize to a variant oligonucleotide probe or be amplified by variant oligonucleotide PCR primers. Alternatively, the oligonucleotides may be designed for use in amplification methods other than PCR. Consequently, one
30 aspect of the present invention is the simultaneous detection and/or identification of various respiratory viruses by targeting nucleic acid sequences which are used as a

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source of specific and ubiquitous oligonucleotide probes and/or amplification primers. Although the selection and evaluation of oligonucleotides suitable for diagnostic purposes require much effort, it is quite possible for the individual skilled in the art to derive, from the selected oligonucleotides (listed in Tables 10 and 11), other
5 oligonucleotides which are suitable for diagnostic purposes.

Thus, the specific primers and/or probes selected for amplification and detection of respiratory viruses and their specific combination in multiplex assays are objects of this invention (Tables 10-13).

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EXAMPLES:

Example 1: Evaluation of different primers for hMPV detection

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An evaluation of the sensitivity of different hMPV primer sets in a real-time PCR assay was performed using 20 positive hMPV cultures grown in LLC-MK2 cells and 10 naso-pharyngeal aspirate specimens. These samples were collected in the Québec City area (QC, Canada) over a period of 3 years (2000-2002). Viral RNA was
20 preably extracted from 200 µl of viral culture supernatants or naso-pharyngeal aspirates using the QIAamp Viral RNA Mini Kit (QIAGEN). Complementary DNA was synthesized using 10 µl of eluted RNA, 0.75 µM of a specific hMPV primer (Table 2, sequences ID Nos. 91, 97, 100, 102, 112), and the Omniscript Reverse Transcriptase Kit (QIAGEN, Mississauga, ON, Canada) following the manufacturer's
25 recommendations. Complementary DNA was amplified using a real-time PCR procedure with the LC Faststart DNA Master SYBR Green 1 Kit (Roche Diagnostics, Laval, QC, Canada) in a LightCycler instrument (Roche Diagnostics). Each reaction had a total volume of 20 µl including 2 µl of RT mixture and 18 µl of a reaction mixture containing 4 mM MgCl₂, 2 µl of Faststart DNA SYBR Green Master Mix,
30 3% DMSO, and 0.5 µM of each hMPV primer (Table 4: sequence ID Nos.: 92 and 94; 100 and 101; 97 and 98; 102 and 103; and 112 and 113, for the nucleoprotein (N),

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matrix (M), fusion (F), phosphoprotein (P), and polymerase (L) genes respectively). Cycling conditions typically included an initial denaturation step of 10 min. at 94°C, followed by 50 cycles of 15 s at 94°C, 5 s at 54°C, and 30 s at 72°C. However, the cycling conditions could slightly vary according to the hMPV gene to amplify.

- 5 Detection of hMPV amplicons was characterized using the melting curve analysis feature of a real-time PCR instrument. Briefly, following the last amplification cycle on a LightCycler instrument, the internal temperature was rapidly increased to 94°C then decreased to 60°C for 30 seconds, followed by slowly increasing to 94°C at a rate of 0.1°C per second, with continuous fluorescence lecture.

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- Using this procedure, the specific melting temperature obtained with the hMPV amplicons produced by the primers specific for target genes coding for N, M, F, P and L proteins was found to be 82.63°C ± 0.87°C, 82.75°C ± 0.80°C, 83.29°C ± 0.45°C, 80.48°C ± 0.46°C, and 77.99 ± 0.33°C, respectively. As shown in Table 5, a real-time
15 PCR assay using primers complementary to the N gene successfully amplified RNA from all 20 cultures and 10 clinical specimens. In contrast, hMPV primers specific for the M, F, P, and L genes had sensitivities of only 70%, 63.3%, 50%, and 89.7% respectively. Thus, primers aimed at amplifying the hMPV N gene appear to target more conserved regions of the hMPV genome and, consequently, were selected for
20 further detailed evaluation (see example 2).

Example 2: Validation of a real-time PCR assay for the hMPV nucleoprotein (N) gene in a pediatric population

- 25 An hMPV N plasmid was constructed by subcloning the amplified hMPV N region in the plasmid pDrive (QIAGEN, Mississauga, ON, Canada). The new plasmid was transcribed using the RNA Transcription Kit (Stratagene, Vancouver, BC, Canada) for sensitivity analysis. Using the previously described RT procedure (N primer, sequence ID No. 91) and real-time PCR protocol (N primers, sequence ID Nos. 92
30 and 94) reported in example 1, the sensitivity of the assay was estimated at 100 copies per reaction with a specific melting temperature of 82 °C. The assay was found to be

specific with no amplification signal observed when viral cultures positive for the human respiratory syncytial virus, the parainfluenza viruses, the influenza viruses A and B, and the adenoviruses were tested. The real-time PCR assay for the hMPV N gene was subsequently validated in a prospective case-control study in children below the age of 3 years hospitalized at Laval University Hospital Center (CHUQ-CHUL) in Québec City, Canada, during the winter season of 2001-02. Cases consisted of children hospitalized for a respiratory syndrome whereas controls consisted of children hospitalized during the same period for a surgery with no respiratory symptoms. At admission, a nasopharyngeal aspirate was collected for viral antigen tests, viral cultures, and RT-PCR studies for influenza A and B viruses, the human respiratory syncytial virus (hRSV), and the hMPV N gene.

No virus was detected in any of the samples from the 51 control children. Among the 208 cases tested by real-time PCR for hMPV, hRSV, influenza A and B viruses, the positivity rates were 5.8%, 51.0%, 21.6%, and 0%, respectively. Viral culture was positive for hMPV in only 2 cases whereas the real-time hMPV PCR assay for the N gene was positive for 12 cases including the 2 positive by viral culture. All positive hMPV PCR results for the N gene were confirmed by a second PCR assay targeting the hMPV fusion (F) gene and by the use of DNA sequencing which indicated the presence of multiple hMPV strains clustering in the two previously-reported F genotypes. Thus, the real-time PCR assay describes in this invention appears to be much more sensitive than conventional viral culture for the detection of hMPV in clinical samples.

Example 3: Typing of hMPV clinical strains using restriction enzyme analysis

We designed a rapid molecular typing method for hMPV epidemiological studies based on amplification of a portion of the fusion (F) gene which is then digested with specific restriction enzymes. Briefly, a 759-bp fragment of the hMPV F gene was
5 amplified by a real-time PCR procedure as described in example 1 using specific primers (sequence ID Nos. 97 and 98). After PCR amplification, two aliquots (10 uL) of the PCR product were digested during 2 hours at 37°C with 10 units of ApaL I and 4 units of Avr II (New England Biolabs, Mississauga, ON, Canada) according to the manufacturer's recommendations. Digested products were then loaded on an 1%
10 agarose gel for electrophoresis.

Table 6 summarizes the size of the F fragments obtained for different hMPV isolates following enzymatic digestion and the corresponding genotype as defined by DNA sequencing and phylogenetic studies. In brief, all hMPV isolates belonging to the
15 genotype F-I were digested by ApaL I (fragments of 532 and 227 bp) but not by Avr II whereas those belonging to the genotype F-II were digested by Avr II (fragments of 447 and 312 bp) but not by ApaL I (see Figure 2 for an example of the band pattern following electrophoresis on an agarose gel).

20 **Example 4 : A prospective case-control study for defining the role of respiratory viruses in children hospitalized for acute respiratory tract infections**

Summary

The human metapneumovirus (hMPV) is a new paramyxovirus recently isolated from
25 young children with respiratory syndromes. The objectives of this study were to estimate the relative contribution of hMPV in children's hospitalization for acute respiratory tract infections (ARTI) and to define its clinical presentation and seasonal pattern.

We evaluated the percentage of hospitalizations for ARTI in children aged 0-3 years attribute to hMPV and other respiratory viruses in a prospective case-control study during the winter/spring seasons of 2002. We used multiplex real-time PCR assays and other conventional diagnostic methods to detect hMPV, the human respiratory syncytial virus (hRSV), and the influenza viruses in nasopharyngeal aspirates of children.

HMPV was detected in 12 (5.8%) of the 208 children hospitalized for ARTI as compared to 118 (56.7%) for hRSV and 49 (23.6%) for influenza A. In contrast, none of the 51 controls harbored any of the respiratory viruses. Most hRSV and influenza infections occurred in January and February whereas the peak hMPV activity was in March and April. The peak age for hospitalizations for hRSV and hMPV infections was < 3 months and 3-5 months, respectively. Diagnoses of bronchiolitis and pneumonitis were made in respectively 67% and 17% of hMPV-infected children compared to 84% and 25% for those with hRSV infection. None of the hMPV-infected children was admitted to the intensive care unit compared to 15% for those with hRSV or influenza A infections.

HMPV causes significant morbidity in young children and its clinical presentation is similar although less severe than that of hRSV.

Introduction

The human metapneumovirus (hMPV) is the first human member of the new *Metapneumovirus* genus within the *Paramyxoviridae* family (van den Hoogen BG, de Jong JC, Groen J, et al. Nat Med 2001;7:719-24; van den Hoogen BG et al. Virology 2002;295:119-32.) The human respiratory syncytial virus (hRSV) belongs to a separate genus within the same family (Taxonomy V. Seventh Report of the International Committee on Taxonomy of Viruses. Academic, San Diego, 2000.).

HMPV has been recently identified in nasopharyngeal aspirates of children and adults suffering from a range of respiratory tract infections in various parts of the world (van

den Hoogen BG, de Jong JC, Groen J, et al. Nat Med 2001;7:719-24; Nissen MD, et al. Med J Aust 2002;176:188; Peret TC, Boivin G, Li Y, et al. J Infect Dis 2002;185:1660-3; Stockton J, et al. Emerg Infect Dis 2002;8:897-901). The clinical syndrome of the infected children encompasses mild respiratory problems to
5 bronchiolitis and pneumonitis (van den Hoogen BG, de Jong JC, Groen J, et al. Nat Med 2001;7:719-24; Pelletier G, et al. Emerg Infect Dis 2002;8:976-8; Boivin G, Abed Y, Pelletier G, et al. J Infect Dis 2002;186:1330-4).

Using reverse-transcription polymerase chain reaction (RT-PCR), the rate of hMPV
10 detection in nasopharyngeal aspirates (NPA) of pediatric patients with unexplained ARTI varied between 1.5 and 10% (van den Hoogen BG, de Jong JC, Groen J, et al. Nat Med 2001;7:719-24; Nissen MD, et al. Med J Aust 2002;176:188). These retrospective studies are small, excluded patients who tested positive for other viruses, only superficially describe the clinical features of the disease and lack
15 morbidity/mortality data. In absence of a control group, these studies cannot differentiate if hMPV is a colonizing or a pathogenic virus. More recently, Stockton et al. identified hMPV RNA in 2.2% of 405 specimens from patients with influenza-like illnesses who consulted general practitioners in England although few swabs were collected from children < 5 years (Stockton J, et al. Emerg Infect Dis 2002;8:897-
20 901).

The objectives of this study were to estimate the relative contribution of hMPV in children's hospitalization for acute respiratory tract infections (ARTI) and to define its clinical presentation and seasonal pattern.

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Materials and Methods

Study design. Participants were children aged ≤ 3 years hospitalized between December 15, 2001 and April 20, 2002 at Laval University Hospital Center (CHUQ-CHUL) in Québec City, Canada. Cases were admitted for an ARTI (bronchiolitis, pneumonia, laryngotracheobronchitis, etc...) whereas controls were hospitalized for an elective surgery and had no respiratory symptoms or fever. Children hospitalized twice were counted as two cases. At admission, after signed consent was obtained from their parents, all children had an NPA (1-2 ml) collected and tested for hRSV antigen (TestPack, Abbott Laboratories, Abbott Park, IL). The specimen was frozen at -80°C until subsequent RT-PCR studies. Additionally, viral cultures, direct immunofluorescence staining, and microbiological testing were performed according to the treating physician. A standardized questionnaire was completed at admission by a single research nurse with the parents. At the end of the hospitalization, the children's charts were reviewed to collect clinical and laboratory data. The study was approved by the CHUQ-CHUL research ethics board.

RNA extraction and cDNA synthesis. Viral RNA was extracted from 200 µl of NPA specimens using the QIAamp viral RNA Mini Kit (QIAGEN, Mississauga, ON, Canada). Complementary cDNA was synthesized using 10 µl of eluted RNA and the Omniscript Reverse Transcriptase kit (QIAGEN). Random hexamer primers (Amersham Pharmacia Biotech, Baie d'Urfé, QC, Canada) were used in the RT step of the multiplex respiratory PCR assay whereas a specific primer (5'-TGGGACAAGTGAAAATGTC-3') serves to synthesize hMPV cDNA in a separate PCR assay. An internal control (300 copies) consisting of a 534-bp transcribed region of the pDrive plasmid (QIAGEN) flanked by influenza B complementary primer sequences (see below) was spiked in the RT reaction of the multiplex respiratory PCR assay to verify the presence of PCR inhibitors.

RT-PCR assays and phylogenetic studies. The multiplex respiratory PCR assay was designed to amplify conserved regions of the influenza A (SEQ. ID Nos.139-140) (Fouchier RA, et al. J Clin Microbiol 2000;38:4096-101) and B (SEQ. ID Nos. 141-

142) (Li J, Chen S, Evans DH. J Clin Microbiol 2001;39:696-704) matrix genes as well as the fusion gene of hRSV (SEQ. ID Nos. 143-144) (Mazzulli T, Peret TC, McGeer A, et al. J Infect Dis 1999;180:1686-9).

- 5 Complementary DNA was amplified using a real-time PCR procedure with the LC Faststart DNA Master SYBR Green 1 Kit (Roche Diagnostics, Laval, Québec, Canada) in a LightCycler instrument (Roche Diagnostics). Each reaction had a total volume of 20 µl including 2 µl of cDNA and 18 µl of a reaction mixture containing 2.4 mM MgCl₂, 2 µl of Faststart DNA SYBR Green Master Mix, 3% DMSO, 0.3 mM
- 10 each of influenza A and B primers, and 0.8 mM of hRSV primers. The thermal cycling incubations consisted of an initial denaturation step at 94°C for 10 min, followed by 50 cycles of 15 s at 94°, 5 s at 58°C, and 25 s at 72°C. At the end of each cycle, the fluorescent signal was measured at a wavelength of 530 nm using the LightCycler Fluorimeter. The melting curve analysis program of the LightCycler was
- 15 used to identify specific PCR products of influenza A (T_m: 85°C), influenza B (T_m: 83°C), hRSV (T_m: 79°C), and the internal control (T_m: 92°C). The sensitivity of the multiplex respiratory PCR assay was estimated at 50 copies for each viral target when mixed with 300 copies of the internal control.
- 20 A specific PCR assay was designed for amplification of the hMPV Nucleoprotein (N) gene in the LightCycler instrument. The sequences of the forward (MPV-NCS) and reverse (MPV-NCA) primers were respectively 5'-GAGTCTCAGTACACAATTAA-3' (SEQ ID NO 92) and 5'-GCATTTCCGAGAACACAC-3' (SEQ ID NO 94). The specific cDNA was amplified using conditions similar to those of the multiplex
- 25 respiratory PCR assay except that 0.5 mM of each primer was added to the master mix. Cycling conditions included an initial denaturation step of 10 min at 94°C, followed by 50 cycles of 15 s at 94°C, 5 s at 54°C, and 30 s at 72°C. The melting temperature of the amplified hMPV N fragment was 82°C and the sensitivity of the PCR assay was 100 copies. For phylogenetic studies, nucleotide sequences were
- 30 determined from amplified hMPV F (fusion) gene products then analyzed using the

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neighbor joining algorithm and Kimura-2 parameters. (Boivin G, Abed Y, Pelletier G, et al. J Infect Dis 2002;186:1330-4).

- hMPV in the general population. To further assess the seasonal distribution, affected age groups and frequency of hMPV, we compared data from the study to those of the general population derived from the viral cultures found positive for hMPV in our regional virology diagnostic laboratory, the only one performing viral cultures for the Québec City area (population approximately 600 000). Respiratory specimens were inoculated in 96-well plates containing ten cell lines (MDCK, LLC-MK2, Hep-2, human foreskin fibroblast, Vero, mink lung, A-549, rhabdomyosarcoma, 293, and HT-29) then incubated for a period of 21 days. A positive cytopathic effect was confirmed by immunofluorescence testing using monoclonal antibodies or by RT-PCR (hMPV).
- 1.5 Statistical analyses. Proportions were compared by the χ^2 test.

Results

The study population included a total of 208 hospitalized cases with ARTI (including 8 children who were admitted twice) and 51 children who served as controls.

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Description of the study population and viral etiologies. The age distribution of children with ARTI is presented in Fig. 3: 56% (116) were male and 44% (92) were female. Hospitalization was the highest in infants ≤ 3 months of age and steadily decreased thereafter. Most (90%) children had no underlying medical conditions at admission.

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All 208 cases had an NPA. The mean delay between the onset of symptoms and collection of NPA was 6 days (median 4 days). This delay did not differ for the different viruses detected. All 208 cases were tested by PCR, 204 had an hRSV

antigen detection test, 100 had a direct examination procedure for other viruses, and 100 had a viral culture. At least one respiratory virus was detected in 164 (79%) cases whereas none was detected in 44. Twelve children (5.8%) were positive for hMPV, 118 (56.7%) for hRSV, 49 (23.6%) for influenza A, and none for influenza B (Table 7). There was no PCR testing for adenoviruses and PIV type 2 but these two viruses were found in 6% and 2%, respectively, of the 100 viral cultures or antigenic assays. Single virus infections occurred in 141 (86%) of the 164 positive cases and mixed infection was present in 23 (14%). Two of the 12 hMPV infections were mixed (hMPV-influenza and hMPV-hRSV). The other combinations were hRSV-influenza A (18 cases), hRSV-adenovirus (2), and influenza A-adenovirus (1).

Among the 208 cases tested by PCR for hMPV, hRSV, influenza A and B viruses, the positivity rates were 5.8%, 51.0%, 21.6%, and 0%, respectively (Table 7). In addition, 16 other cases had one of the four latter respiratory viruses identified only by culture (3 influenza A and one hRSV), only by an antigen detection test (10 hRSV and one influenza A) or by both culture and antigen detection test (1 hRSV). Among the 8 children hospitalized twice, none had the same viral infection at both admissions. The combinations observed were hMPV - hRSV (2), hMPV - no virus (1), hRSV - no virus (2), hRSV - influenza (2), no virus - no virus (1).

The biweekly distribution of cases with respiratory tract viruses is shown in Fig. 4. hRSV and influenza A infections occurred predominantly between January and March, whereas hMPV infections occurred mostly in March and April. The proportion of children with virologically-confirmed respiratory tract infection decreased after February.

Clinical features of cases. The distribution of the age distribution by different viral infections is shown in Fig. 3. While the peak age for hMPV infection was 3-5 months, it was before 3 months for hRSV infection. For influenza A, it spread evenly during the first year of life. The peak age for mixed infection was 6-11 months and decreased thereafter. Gender was distributed evenly with each virus group but more males

(70%) had mixed viral infections. The majority (75% with hMPV, 93% with hRSV, 90% with influenza A virus infection) of the children in different etiological groups had no medical underlying conditions. Three (25%) children with hMPV infection had a cardiac disorder, one having concomitant cardiac, pulmonary, and neurological problems.

Signs and symptoms recorded with the different respiratory viruses were generally similar except for the vomiting which occurs more frequently with hMPV infections ($p = 0.05$) (Table 8). The mean and median duration of hospitalization was similar for hMPV, hRSV and influenza A viruses being respectively 5.5 and 4.5, 5.8 and 5.0, and 4.9 and 4.0 days. Of note, one third of hMPV-infected children were hospitalized more than 7 days. None of the children with hMPV infection was admitted to the intensive care unit (ICU) contrasting with 15% and 16% of children with hRSV and influenza A, respectively. There was no death as part of this study. The duration of the hospitalization in children with no detectable virus was shorter than that in children with single or mixed infection (Kruskal-Wallis Test, $p < .0001$). Two-thirds of the children were given antibiotics during their hospitalization, independently of the etiology of their respiratory disease.

At hospital discharge, a final diagnosis of bronchiolitis was given to 67% of children with hMPV, 84% with hRSV, and 51% with influenza A ($p < 0.001$) (Table 9). Otitis occurred in about half of children with hMPV, hRSV, and influenza A infections. Pneumonitis was less frequently diagnosed in children with hMPV compared to those with hRSV or influenza A (17%, 25%, and 37%, $p=0.22$). Final diagnoses were similar with single and mixed infections.

Controls. There were 51 children in the control group, 29 (56.9%) males and 22 (43.1%) females. The age distribution of the controls was similar to that of the cases (Fig. 3) as was the period of hospital admission (Fig. 4). None of the controls had a virus detected by PCR.

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hMPV in the general population. The regional virology laboratory received 1505 respiratory specimens for viral culture between January 1 and June 30, 2002. In total, 36 (including two study participants) or 2.9% were positive for hMPV: 24 (66.6%) in children < 2 years of age, 5 in those 2 to 4 years, 4 in adults 30-49 years, and 3 in those 70 years or older. Most cases (81%) were isolated over a two-month period (from March 23 to May 18) (Fig. 5). When comparing the seasonal distribution of hMPV in hospitalized children (study population) and in the general population, it appears that the study in hospitalized children did not cover the entire hMPV season as it was stopped just after the peak time of hMPV transmission (April 6-20).

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Phylogenetic analyses of hMPV strains. The 12 hMPV strains isolated in the prospective study clearly clustered into two F lineages with nine strains belonging to group 1 and three to group 2 (Fig. 6). Seven of the 9 group 1 strains had identical F gene sequences. At the nucleotide level, there was 84-85% similarity between groups versus 98-100% (group 1) and 93-99% (group 2) similarity within groups. There were fewer differences at the amino acid level i.e. 94-96% similarity between groups versus 99-100% (group 1) and 98-99% (group 2) among strains within the same group. Although there was a trend for more recent strains to cluster in group 2, the correlation between genotypes and date of hospitalization was not perfect as two strains detected on the same day (No. 216 and 217) belonged to two different F lineages.

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Discussion

Our prospective study has revealed important clinical and epidemiological features related to hMPV. First, our data indicate that hMPV is really a respiratory pathogen. Second, we found that it contributes to ARTI leading to children's hospitalization in proportion similar to adenoviruses or PIV but significantly less than hRSV and influenza viruses. Third, the symptoms and complications associated with hMPV were indistinguishable from those caused by hRSV. Finally, our results suggest that the epidemiology of hMPV infection in children may differ from that of hRSV and

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influenza viruses both in terms of the age of first acquisition and in the timing of the seasonal epidemics.

Recent studies by our group (Pelletier G, et al. *Emerg Infect Dis* 2002;8:976-8; Boivin G, Abed Y, Pelletier G, et al. *J Infect Dis* 2002;186:1330-4) and others (van den Hoogen BG, de Jong JC, Groen J, et al *Nat Med* 2001;7:719-24.; Nissen MD et al. *Med J Aust* 2002;176:188; Stockton J, et al. *Emerg Infect Dis* 2002;8:897-901) had suggested that hMPV should be added to the list of human respiratory viral pathogens (Dowell SF, Anderson LJ, Gary HE, Jr., et al. *J Infect Dis* 1996;174:456-62; Treanor JJ. Respiratory Infections. In: Richman DD, Whitley, R.J., Hayden, F.G., ed. *Clinical Virology*. Vol. 1. Washington: ASM Press, 2002:7-26).

The absence of hMPV in respiratory tract of our 51 control children, the absence of other respiratory viruses in 83% of the 12 hMPV-infected children and the severity of their symptoms (bronchiolitis and/or pneumonitis) provide further evidence that hMPV is really a pathogenic respiratory virus. The absence of underlying medical conditions in 75% of the hMPV-infected children further demonstrates its pathogenicity. The use of PCR assays was particularly advantageous for hMPV because its growth in culture is fastidious and limited to a few permissive cell lines (Boivin G, Abed Y, Pelletier G, et al. *J Infect Dis* 2002;186:1330-4) and because rapid antigenic detection tests are currently unavailable.

Our study provides for the first an estimate of the proportion of ARTI hospitalizations attributable to hMPV in a pediatric population. During the period ranging from December 15 to April 20 2002, hMPV accounted for 5.8% of all hospitalizations for respiratory tract infections in children aged 0-3 years. This underestimates the real proportion as our hospitalization study stopped before the end of the hMPV season prevailing in the community (Fig. 5). Although we did not perform PCR testing for adenoviruses and PIV, the percentage of hospitalizations caused by hMPV seems similar to that attributable to these two viruses and much smaller than that of hRSV or influenza A.

One of the most important conclusion of our study is that hMPV disease cannot be distinguished on clinical findings from that caused by hRSV and influenza A (Tables 8 and 9) but tended to be somewhat less severe with fewer pneumonia and no admission in the ICU. Nevertheless, hMPV infection was associated with a significant clinical and economical burden as shown by a mean hospital stay of 5.5 days and one-third of hMPV-infected cases being hospitalized for > 7 days.

A small serological study from the Netherlands showed that all children over the age of 5 years had hMPV antibodies suggesting a high level of transmission.¹ Data from our study suggest that morbidity caused by hMPV is greatest in children < 2 years of age as they represented 83% (10/12) of our hospitalized cases and two-thirds of the hMPV isolates recovered in our diagnostic virology laboratory. This suggests that similar to other paramyxoviruses such as hRSV, the morbidity of hMPV in children occurs through primo-infection. In contrast to hRSV which peaked during the first three months of life, hMPV infections peaked at a slightly older age i.e. between the third and fifth month of life. Whether this difference depends on a longer persistence of maternal antibodies or a less efficient transmission mode in the case of hMPV would require additional studies.

During the 4-week period from mid-March to mid-April, hMPV infections clustered (11/12 detected) and accounted for 18.9% of all hospitalizations for ARTI in children. This contrasts with hRSV and influenza A which occurred mostly in January and February (Figure 4). Based on passive surveillance data from our regional virology laboratory, the peak time of hMPV transmission in the community occurred between April 6-20, 2002, and continued beyond the end of our study in hospitalized children (Fig. 5). Year-long active surveillance studies will be required to better assess the seasonal patterns of hMPV transmission.

As described for hRSV (Mazzulli T, Peret TC, McGeer A, et al J Infect Dis 1999;180:1686-9), several strains of hMPV circulated during a very short period of

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time (one month) in our study area. The hMPV strains segregated into two F subgroups in agreement with previous studies although one strain clearly predominated accounting for 58.3% of all isolates (van den Hoogen BG, de Jong JC, Groen J, et al. Nat Med 2001;7:719-24; Peret TC, Boivin G, Li Y, et al. J Infect Dis 2002;185:1660-3; Boivin G, Abed Y, Pelletier G, et al. J Infect Dis 2002;186:1330-4).

Due to the small number of hMPV strains belonging to one of the F subgroup, we did not attempt to correlate hMPV genotype with clinical outcome. Such viral heterogeneity may allow multiple reinfections throughout life especially in elderly subjects and immunocompromised patients (Pelletier G, Dery P, Abed Y, Boivin G Emerg Infect Dis 2002;8:976-8).

In conclusion, our study supports the concept of the epidemic nature of hMPV infection and establishes its role as a significant pathogen in severe ARTI of children.

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Example 5: Determination of the hMPV Load in Clinical Samples Using Quantitative Real-time PCR

20 An evaluation of a quantitative real-time PCR hMPV assay using a TaqMan probe was performed using naso-pharyngeal aspirate specimens collected from children and adults in Québec City during the winter seasons of 2001-02 and 2002-03. Viral RNA was first extracted from 200 µl of naso-pharyngeal aspirates using the QIAamp Viral RNA Mini Kit (QIAGEN) and eluted in a volume of 40 µl. Serial concentrations
25 (5X10² to 1X10⁹ copies) of a transcribed hMPV plasmid were used to construct the standard curve of the assay. Complementary DNA was synthesized using 10 µl of eluted RNA from clinical samples or hMPV plasmid dilutions, 50 ng (0.75 µM) of random hexamer primers (Amersham Pharmacia Biotech), 0.5 mM of dNTPs, 1X Omniscript buffer and 4 units of the Omniscript reverse transcriptase (QIAGEN) in a
30 final volume of 20 µl. The reverse transcription (RT) mixture was incubated during 1.5 hr. at 37°C and inactivated at 70°C during 10 min. Complementary DNA was amplified by real-time PCR with a TaqMan probe for the hMPV L gene and the LC

Master Hybridization Probe Mix (Roche Diagnostics) in a LightCycler instrument (Roche Diagnostics). Each reaction had a volume of 20 µl including 2 µl of RT mixture, 4 mM MgCl₂, 0.3 µM of specific hMPV L primers (sequence ID Nos. 112 and 114), 0.6 µM of a specific hMPV L probe (SEQ. ID. No. 127), and 2 µl of the LC Master Hybridization Probe Mix (Roche Diagnostics). Cycling conditions included an initial denaturation step of 30 s at 94°C, followed by 60 cycles of 5 s at 94°C, 5 s at 56°C, and 25 s at 72°C. A fluorescence lecture was taken after each elongation step (Fig. 9A). A standard curve for the PCR reaction was constructed by plotting cycle threshold values against log concentrations of each hMPV plasmid dilution. The number of hMPV copies present in clinical samples was calculated by interpolating cycle threshold values into the assay's standard curve (Fig. 9B).

Example 6: Determination of hMPV genotypes based on amplification and sequencing of the viral F and G genes.

Determination of hMPV genotypes was achieved by PCR amplification of the F or G genes followed by DNA sequencing of the viral amplified products. Different sets of primers were used for PCR amplification and DNA sequencing of the F (SEQ. ID. Nos. 97 and 98) and G (SEQ. ID. Nos. 104 and 107 or 108 and 109) genes. Alignment of viral DNA sequences was done with the CLUSTAL W software version 1.7 for Unix and phylogenetic trees were computed by maximum parsimony, distance and maximum likelihood-based criteria analysis using PAUP version 4.0.d8. Phylogenetic trees for both the F (Fig. 10A) and G (Fig. 10B) genes from Canadian and non-Canadian viral isolates revealed the existence of two hMPV groups (genotypes A and B) with two subgroups (subtypes 1 and 2) within each group.

Example 7: Comparison of viral culture and multiplex PCR assay for detection of influenza A virus.

A multiplex PCR assay (including PCR primers defined in SEQ. ID. Nos. 139, 140, 141, 142, 143, and 144) aimed at detecting influenza A and B viruses and the respiratory syncytial virus was used to assess the etiology of severe acute respiratory

tract infections (ARTI) necessitating hospitalization in children aged 0-3 years during the winter season 2001-02 at the CHUL, an university-based hospital, in Québec City (Canada). Nasopharyngeal (NPA) samples from all 208 children with ARTI were tested by multiplex PCR whereas a subset of 100 NPA specimens was inoculated on

5 Madin Darby Canine Kidney (MDCK) cells for influenza culture. Briefly, viral RNA was preably extracted from 200 µl of naso-pharyngeal aspirates using the QIAamp Viral RNA Mini kit (QIAGEN, Mississauga, ON, Canada). cDNA was then synthesized using 10 µl of the RNA preparation, 0.75 µM of random hexamer primers (Amersham Pharmacia Biotech, Baie d'Urfé, QC, Canada), 300 copies of an internal

10 control template, and the Omniscript Reverse Transcriptase Kit (QIAGEN, Mississauga, ON, Canada) following the manufacturer's instructions. The internal control template consisted of a 558-bp transcribed region of an herpes simplex virus type 2 DNA polymerase region flanked by influenza B complementary primer sequences cloned into the pDrive plasmid (QIAGEN). cDNA was amplified using a

15 real-time PCR procedure with the LC Faststart DNA Master SYBR Green 1 Kit (Roche Diagnostics, Laval, QC, Canada) in a LightCycler instrument (Roche Diagnostics). Each reaction had a total volume of 20 µl including 2 µl of complementary DNA and 18 µl of a reaction mixture containing 4 mM MgCl₂, 2 µl of LC Faststart DNA SYBR Green Master 1 Mix, 3% DMSO, 0.3 µM of influenza A

20 and influenza B primers, and 0.8 µM of human respiratory syncytial virus primers (Table 10). Cycling conditions included an initial denaturation step of 10 min. at 94°C, followed by 50 cycles of 15 s at 94°C, 5 s at 58°C, and 25 s at 72°C. Detection of viral amplicons was characterized using the melting curve analysis feature of a real-time PCR instrument. Briefly, following the last amplification cycle on a

25 LightCycler, the reaction temperature was rapidly increased to 94°C and was then decreased to 60°C for 30 seconds followed by a slow increase to 94°C at a rate of 0.1°C per second, with continuous fluorescence lecture. Using this procedure, the amplified products of influenza A, influenza B, hRSV, and the internal control could be differentiated by virtue of their specific T_m values i.e. 85, 83, 79, and 91°C,

30 respectively (Table 13 and Fig. 11).

Influenza A virus was detected by multiplex PCR (specific T_m value of 85°C) in 45/208 (21.6%) of the samples tested whereas the culture was positive for this virus in 14/100 (14%) tested NPA samples from children. For the subset of 100 NPA specimens tested by both methods, 88 (88%) had concordant results (11 positive, 77 negative) whereas discordant results were obtained for 12 (12%) samples (3 culture⁺/PCR⁻, 9 culture⁻/PCR⁺). Assuming that all positive results (by either culture or PCR) were true positive, the sensitivity values of the culture and the multiplex PCR for influenza A virus were 60.9% and 87.0%, respectively. There was no positive result for influenza B virus by any detection method as part of this study.

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Example 8: Comparison of antigen detection and multiplex PCR assay for detection of the human respiratory syncytial virus.

Same as example 1, except that the multiplex PCR assay was used to detect hRSV from NPA samples obtained from 211 children with ARTI and compared with an antigen detection test for hRSV (TestPack, Abbott Laboratories, Abbott Park, IL).

hRSV was detected by the multiplex PCR (specific T_m value of 79°C) in 109/211 (51.7%) of the tested samples whereas the hRSV antigen detection test was positive in 93/211 (44.1%) tested NPA samples from children. Concordant results were found in 183 (86.7%) samples (87 positive, 96 negative) whereas discordant results were obtained for 28 (13.3%) samples (6 antigen⁺/PCR⁻, 22 antigen⁻/PCR⁺). A second RT-PCR assay for detection of another hRSV gene (glycoprotein G) was used to resolve the discrepancies (Peret et al., 1998, J Gen Virol. 79:2221-2229). After the resolution of the discrepant results, the sensitivity values of the antigen detection test and the multiplex PCR for hRSV were 80.5% and 96.5%, respectively.

Example 9: Evaluation of multiplex real time PCR assay for Influenza and human respiratory syncytial viruses.

5 We developed a real-time multiplex PCR assay for influenza viruses and HRSV using the melting curve analysis feature of the LightCycler instrument to rapidly distinguish viral products.

Materials and methods

10 **Study population and antigenic test.** Nasopharyngeal aspirates (NPA) were prospectively collected from children aged 0-3 years hospitalized for ARTI during the winter season 2001-02 at a single, university-based hospital, in Québec City (Canada) (Boivin, G., et al. 2003. Emerg. Infect. Dis. 9:634-640). The study was approved by the institutional review board of the Centre Hospitalier Universitaire de Québec. All samples were tested by the multiplex real-time PCR assay whereas antigen detection
15 tests were performed on a subset of samples upon request by the treating physician. An aliquot (750 µl) of fresh NPA was first tested for the presence of HRSV and influenza A/B antigens using respectively the RSV TestPack (Abbott Laboratories, Abbott Park, IL) and the Directigen Flu A+B test (Becton Dickinson, Sparks, MD). The rest of the specimen was frozen at -80°C for a maximum of 3 months before
20 nucleic acid extraction and PCR testing.

RNA extraction and cDNA synthesis. Viral RNA was extracted from 200 µl of NPA samples using the QIAamp Viral RNA Mini kit (QIAGEN, Mississauga, ON, Canada). Complementary DNA was then synthesized using 10 µl of the RNA preparation, 0.75
25 µM of random hexamer primers (Amersham Pharmacia Biotech, Balc d'Urfé, QC, Canada), and the Omniscript Reverse Transcriptase kit (QIAGEN) in presence of 300 copies of an internal control. The internal control template consisted of a 558-bp transcribed region of the herpes simplex virus type 2 DNA polymerase gene flanked by influenza B complementary primer sequences (see below) cloned into the pDrive
30 plasmid (QIAGEN).

Real-time multiplex and conventional PCR assays. The multiplex PCR respiratory assay was designed to amplify conserved regions of the influenza A (Fouchier, R. A., et al. . 2000.. J. Clin. Microbiol. 38:4096-4101) and B (Li, J., S. Chen, and D. H. Evans. 2001.. J. Clin. Microbiol. 39:696-704) matrix genes as well as the fusion gene of HRSV (Mazzulli, T., et al, 1999. J. Infect. Dis. 180:1686-1689). Complementary DNA was amplified using a real-time PCR procedure with the LC Faststart DNA Master SYBR Green 1 kit (Roche Diagnostics, Laval, QC, Canada) in a LightCycler instrument (Roche Diagnostics). Each reaction had a total volume of 20 µl including 2 µl of cDNA and 18 µl of a reaction mixture containing 2.4 mM MgCl₂, 2 µl of Faststart DNA SYBR Green 1 Master Mix, 3% DMSO, 0.3 mM of influenza A and B primers (SEQ. ID Nos. 139-140 and 141-142), and 0.8 mM of HRSV primers (SEQ. ID Nos. 143-144). Cycling conditions included an initial denaturation step of 10 min at 94°C, followed by 50 cycles of 15 s at 94°C, 5 s at 58°C, and 25 s at 72°C. At the end of each cycle, the fluorescent signal was measured at a wavelength of 530 nm using the LightCycler Fluorimeter. The melting curve analysis program of the LightCycler was used to identify specific PCR products. Briefly, following the last amplification cycle, the reaction temperature was rapidly increased to 94°C and was then decreased to 60°C for 30 s followed by a slow increase to 94°C at a rate of 0.1°C per s, with continuous fluorescence monitoring. For resolution of discrepant results between the multiplex PCR assay and antigenic tests, conventional RT-PCR assays for detection of the glycoprotein G gene of HRSV (Peret, T. C., et al. 1998. J. Gen. Virol. 79:2221-2229) and the M2 gene of influenza A viruses (Klimov, A. I., et al. . 1995. J. Infect. Dis. 172:1352-1355) were performed retrospectively.

Results

Assay's characteristics. The sensitivity of each individual real-time PCR assay and of the multiplex PCR respiratory assay was determined for each target by testing serial dilutions of transcribed plasmids containing specific viral sequences. The lower limit of detection for influenza A, influenza B, and HRSV was found to be 10, 50 and 50 copies, respectively, in individual PCR assays whereas it was 50 copies for each target (10 out of 10 times for influenza A and 9 out of 10 times for influenza B and

HRSV) in the multiplex PCR test. No amplification signal was detected in the real-time multiplex assay when testing viral DNA or RNA from adenoviruses, rhinoviruses, enteroviruses (echo 11), parainfluenza viruses 1-3, human metapneumovirus, and herpesviruses (herpes simplex virus type 1 and 2, cytomegalovirus, and varicella-zoster virus). Specific melting temperature (T_m) values were first determined by testing a set of clinical isolates and vaccine strains (11 influenza A/H1, 10 influenza A/H3, 10 influenza B, and 17 HRSV) from different years (Table 14). A representative set of results is shown in Fig.11. The mean T_m values were 85.27 ± 0.22 , 83.47 ± 0.46 , and 79.51 ± 0.30 °C for influenza A, influenza B, and HRSV corresponding to fragments of 245, 524, and 380 bp, respectively, after gel electrophoresis (Table 14). We found no influence of influenza A subtype (H1 and H3) and HRSV genotype (A and B) on the T_m values (Table 14). The addition of 300 copies of the internal control in the assay's master mix resulted in a specific amplification peak with a T_m value of 91°C (558 bp) in the absence of amplified viral products.

Evaluation of the multiplex PCR respiratory assay in a pediatric population. The multiplex PCR assay was evaluated using extracted RNA from 208 NPA samples collected during a prospective pediatric study aimed at assessing the role of the human metapneumovirus in hospitalized children (0-3 years) with ARTI (Boivin, G., et al. 2003. *Emerg. Infect. Dis.* 9:634-640). The number of positive samples by multiplex PCR for influenza A, influenza B, and HRSV was found to be 45 (21.6%), 0 (0%), and 106 (51.0%), respectively. Overall, the rate of positivity for any of the 3 viruses was 66.8% (139/208) including 5.8% (12/208) of co-infections with influenza A and HRSV. None of the samples was considered to contain PCR-inhibitory samples as verified by the amplification of the internal control in all PCR-negative samples. The ranges of T_m values for influenza A- and HRSV-positive samples were 85.10 ± 0.39 and 79.60 ± 0.42 °C, respectively. All amplified products with one of the latter T_m values were confirmed as specific viral targets by visualizing the appropriate band on agarose gel. As none of the samples contained influenza B virus sequences (which correlates with the very occasional isolation of influenza B viruses in the Québec City

area during the 2001-2002 season), a clinical evaluation of the multiplex PCR assay was conducted for influenza A and HRSV only.

Evaluation of the multiplex PCR respiratory assay for detecting influenza A virus. From the 208 NPA evaluated by multiplex PCR, a subset of 172 samples were also tested for the presence of influenza antigens using the Directigen Flu A+B test (Table 15). Concordant results were obtained for 145 (84.3%) samples including 17 positive and 128 negative results by the two tests. A total of 27 (15.7%) samples showed discordant results with 25 being positive by the multiplex PCR assay only and two positive by the antigenic test only. In order to resolve the discrepant results, a second RT-PCR test targeting a conserved gene (M2) of influenza A viruses was performed as reported (Klimov, A. I., et al. . 1995. J. Infect. Dis. 172:1352-1355). As shown in Table 15, influenza A virus M2 sequences were detected by the conventional RT-PCR assay in 22 (81.5%) of the 27 discordant samples. Using the M2 RT-PCR assay as the reference test, the sensitivity, specificity, positive predictive and negative predictive values of the multiplex real-time PCR assay and the antigenic test for influenza A virus were 100%, 97.7%, 92.8%, 100% and 43.6%, 98.5%, 89.5%, 85.6%, respectively. The multiplex PCR respiratory assay was positive for HRSV in 12 (44.4%) of the 27 discordant influenza A samples with 10 of these samples showing dual HRSV/influenza A infections by the multiplex PCR assay (Table 16). The mean cycle threshold (C_T) values, which are inversely correlated with the amounts of viral RNA, were 28.1 and 33.0 for PCR-positive/antigen-positive and PCR-positive/antigen-negative samples, respectively (Table 16). These values correspond to approximately 5000 and 50 copies, respectively, when a specific influenza A plasmid was tested in the multiplex PCR assay.

Evaluation of the multiplex PCR respiratory assay for detecting HRSV. A total of 204 NPA samples could be evaluated by both the multiplex real-time PCR assay and the presence of HRSV antigens using the RSV TestPack (Table 17). Concordant results were found in 172 (84.3%) samples including 83 positive and 89 negative results by the two tests. Thirty-two (15.7%) samples had discordant results with 21

being positive by the multiplex PCR assay only and 11 by the antigenic test only. Conventional RT-PCR tests for the HRSV glycoprotein G (A and B subtypes) were performed as previously described (Peret, T. C., et al. 1998. *J. Gen. Virol.* 79:2221-2229) to resolve discrepant results. Specific sequences were detected by RT-PCR assays for the HRSV glycoprotein G gene in 26 (81.2%) of the 32 discordant samples including 11 A and 15 B strains (Table 18). Using the latter test as "gold standard", the sensitivity, specificity, positive predictive and negative predictive values of the multiplex real-time PCR assay and the antigenic test for HRSV were 94.5%, 98.9%, 99.0%, 94.0% and 81.6%, 94.7%, 94.7%, 81.8%, respectively. Four (66.7%) of the six false-negative HRSV results by multiplex PCR were positive for influenza A (Table 18). The mean C_T values of the PCR-positive/antigen-positive and PCR-positive/antigen-negative samples were 28.6 and 32.7, respectively (Table 18). These values correspond to approximately 1000 and 100 copies, respectively, when a specific HRSV plasmid was tested in the multiplex PCR assay.

Discussion

In this report, we describe a new multiplex real-time PCR assay for the most commonly detected respiratory viral pathogens, namely influenza viruses (A and B) and HRSV. The key features of this novel assay include its rapidity (turnaround time of approximately 2h30 including 30 min for sample preparation, 60 min for RT and 60 min for real-time PCR including viral identification), and its sensitivity (50 copies per assay for each viral target). Our results clearly demonstrate that our multiplex real-time PCR assay is more sensitive than commercially-available antigenic detection tests for both influenza A and HRSV with the greatest difference in sensitivity noted for influenza viruses.

Multiplex RT-PCR assays targeting up to nine different respiratory pathogens have been previously reported (Fan, J., K. J. Henrickson, and L. L. Savatski. 1998. *Clin. Infect. Dis.* 26:1397-1402, Grondahl, B., et al. 1999. *J. Clin. Microbiol.* 37:1-7, Kehl, S. C., et al. 2001. 39:1696-1701, Osiowy, C. 1998. *J. Clin. Microbiol.* 36:3149-3154, Stockton, J., et al. 1998. *M J. Clin. Microbiol.* 36:2990-2995, Valassina, M., A. M.

Cippone, M. G. Cusi, and P. E. Valensin. 1996. *Clin. Diag. Virol.* 8:227-232). More recently, a TaqMan-based real-time PCR assay for simultaneous detection of influenza A and B viruses has also been described (van Elden, L. J., et al. 2001. *J. Clin. Microbiol.* 39:196-200). Compared to conventional multiplex PCR assays, our
5 real-time PCR test is much more rapid because it avoids additional nested amplification and/or hybridization steps required for identification of viral products. Furthermore, the real-time amplification procedure minimizes the chances of contamination because there is no post-PCR processing of the samples. Although our multiplex real-time PCR assay based on melting curve analysis of amplicons does not
10 permit absolute quantification of the viral targets as in the TaqMan PCR procedure (van Elden, L. J., et al. 2001. *J. Clin. Microbiol.* 39:196-200), it allows for a larger number of viral targets to be simultaneously detected since there is no limitation related to the capability of the system to detect multiple dyes linked to detection probes with distinct emission wavelengths. Eventually, more than three viral targets
15 could be simultaneously detected in the LightCycler assay assuming the absence of interaction between PCR primers and a reproducible and discriminative T_m value for each viral amplicon.

Evaluation of our multiplex real-time PCR assay in a pediatric population with severe
20 ARTI clearly illustrated its clinical potential. Indeed, our assay identified a viral pathogen (influenza or HRSV) in two-thirds of the hospitalized children. These numbers are similar to the ones previously reported by our group in the same population using individual real-time assays for these viral pathogens (Boivin, G., et al. 2003. *Emerg. Infect. Dis.* 9:634-640). Notably, we were able to show that 6% of
25 hospitalized children had dual viral infections, a finding that has been reported albeit at a lower frequency by other investigators (Grondahl, B., et al. 1999. *J. Clin. Microbiol.* 37:1-7, Kehl, S. C., et al. 2001. 39:1696-1701, Osiowy, C. 1998. *J. Clin. Microbiol.* 36:3149-3154). Rapid identification of these viral pathogens (influenza and HRSV) is of paramount importance for isolation purposes in the hospital setting
30 and early institution of specific antiviral therapy (Whitley, R. J., et al. 2001. *Pediatr. Infect. Dis. J.* 20:127-133). We are currently designing additional multiplex assays

based on the same technology to cover the whole spectrum of respiratory pathogens including parainfluenza viruses (PIV), adenoviruses, enteroviruses, and coronaviruses (Treanor, J. 2002. Respiratory Infections, p. 7-26, In Richard J. Whitley, Douglas D. Richman and Frederick G. Hayden (eds.), Clinical Virology, 2nd ed. ASM Press, Washington, D.C.). To this list, we should also add the recently described human metapneumovirus which has been reported by our group and others in up to 10% of ARTI in hospitalized children (Boivin, G., et al, 2003. Emerg. Infect. Dis. 9:634-640, Jartti, T., B. van den Hoogen, R. P. Garofalo, A. D. Osterhaus, and O. Ruuskanen. 2002.. Lancet. 360:1393-1394, Nissen, M. D., et al 2002. Med. J. Aust. 176:188, van den Hoogen, B. G., J. C. de Jong, J. Groen, T. Kuiken, R. de Groot, R. A. Fouchier, and A. D. Osterhaus. 2001.. Nat. Med. 7:719-724):

A specific evaluation of the real-time multiplex PCR assay for influenza A revealed that it was twice as sensitive as the rapid antigen detection test in use at our institution during the winter season of 2001-2002. None of the two PCR-negative, antigen-positive samples were confirmed by a second PCR targeting another conserved gene (M2) of influenza A whereas most (22/25, 88.0%) multiplex PCR-positive, antigen-negative were. In general, the false-negative antigenic test results could be explained by low amounts of viral RNA in those NPA samples as demonstrated by high C_T values in the corresponding real-time PCR assays. Three multiplex PCR test results were not confirmed by the influenza A M2 PCR test and were thus considered false-positive results. However, as we have not formally evaluated the sensitivity of the M2 PCR test and since viral cultures were not routinely done, we cannot rule out the possibility that such discrepant results were indeed true positive. We and other investigators have shown the superiority of RT-PCR tests over conventional methods (antigenic tests and viral culture) for detecting influenza viruses in clinical samples including those sent to the laboratory by mail (Boivin, G., I. Hardy, and A. Kress. 2001. J. Clin. Microbiol. 39:730-732, Ellis, J. S., D. M. Fleming, and M. C. Zambon. 1997. 1996. J. Clin. Microbiol. 35:2076-2082, Kehl, S. C., et al. 2001. 39:1696-1701, Steininger, C., et al. 2002. J. Clin. Microbiol. 40:2051-2056, van Elden, L. J., et al. 2001. J. Clin. Microbiol. 39:196-200). It is now common procedure at our institution

to confirm any negative antigenic tests results for influenza A and B by either viral culture or RT-PCR considering the high specificity but relatively poor sensitivity of the former assays.

- 5 For HRSV, the multiplex real-time PCR assay was also found to be more sensitive (by approximately 15%) than the rapid antigenic test when a second RT-PCR assay for the HRSV gG gene was used to resolve the discrepancies. Most of the false-negative antigenic test results could be explained by low amounts of viral RNA in the NPA samples as shown by mean C_T values of 32.7 for discordant results compared to
10 28.6 for concordant positive results. The specificity of the multiplex assay was excellent with only one positive result not confirmed by the second PCR test. In contrast, the multiplex PCR assay missed six cases of HRSV which tested positive in both the antigenic test and the second PCR assay for HRSV gG. Notably, four of those six samples tested positive for influenza A in the multiplex PCR assay. Thus,
15 although our multiplex PCR test has the capability of detecting dual infections (as seen in 6% of our cases), it is possible that high amounts of one virus could inhibit amplification of other pathogens. It is noteworthy that the multiplex PCR assay had the ability to amplify both HRSV genotypes as shown by the detection of 15 B and 11 A genotypes using specific PCR assays aimed at detecting variable regions of the
20 HRSV gG gene (Mazzulli, T., et al, 1999, *J. Infect. Dis.* 180:1686-1689). Although the rapid antigenic test had a relatively good performance (sensitivity: 82%, specificity 95%) for detection of HRSV in young children, the real advantage of PCR probably resides in the adult population where viral titers are lower and where antigenic tests are not recommended with upper respiratory tract samples (Englund, J.
25 A., et al 1996., 34:1649-1653).

- There are some limitations to our study which are worth mentioning. First, the absence of circulation of influenza B viruses during the study period prevents adequate validation of our multiplex assay for this pathogen and in particular for its
30 ability to detect mixed (influenza B and HRSV) infections. Second, the performance of our multiplex PCR assay cannot be generalized to other types of samples (throat

swabs, sputum) and to other populations (outpatients, adults) at the present time. Also, the absence of serological testing in our study may have underestimated the rate of viral infections especially for those children who presented late after the onset of symptoms. Finally, although it was relatively easy to discriminate between the different viral pathogens based on their specific T_m values only (Table 14), we sometimes had to confirm viral amplicons by gel electrophoresis, which increases the assay's turnaround time.

In conclusion, we described a rapid and sensitive multiplex real-time PCR assay for detecting influenza viruses and HRSV in children's NPA samples. This new assay is as specific and much more sensitive than currently-available antigen detection tests and could complement the latter in the hospital setting when there is high clinical suspicion despite negative results. Future work is needed to expand the panel of viral pathogens detected by such rapid molecular methods in order to eventually circumvent the need for viral cultures. Also, future evaluation of the multiplex PCR assay is warranted in the adult population with severe ARTI.

Example 10 : Description and Evaluation of the Multiplex Respiratory-1 PCR.

5 Same as example 9, except that hMPV primers (as defined in SEQ. ID. Nos. 95 and 96 or 112 and 114) were added to the multiplex PCR assay (already containing primers of SEQ. ID. Nos. 139+140 for influenza A, 141+142 for influenza B, and 143+144 for hRSV) at a concentration of 0.3 μ M. The cycling conditions included an amplification step of 50 cycles of 15 s at 94°C, 5 s at 58°C, and 28 s at 72°C. The T_m values determined with the LightCycler instrument were 91°C, 85°C, 83°C, 79°C, and 82°C/77°C for the internal control, influenza A, influenza B, hRSV, and hMPV N/L genes, respectively (Fig. 7A for hMPV N primers of SEQ. ID. Nos. 95 and 96 and Fig. 7B for hMPV L primers of SEQ. ID. Nos. 112 and 114). The lower limit of detection of the multiplex respiratory-1 PCR was 10, 50, 100, and 100 copies for influenza A, influenza B, hRSV, and hMPV, respectively, in the presence of 500 copies of an internal control (plasmid flanked by influenza B complementary primer sequences). The multiplex respiratory-1 assay was found to be specific with no amplification of adenoviruses, enteroviruses, rhinoviruses, parainfluenza viruses 1-3, coronaviruses, herpes simplex virus type 1 and 2, varicella-zoster virus, cytomegalovirus, HHV-6, HHV-8, and Epstein-Barr virus.

10 The multiplex respiratory-1 PCR was evaluated with NPA samples from 248 children ≤ 3 years with acute respiratory tract infections and 108 adults ≥ 50 years with exacerbation of chronic obstructive pulmonary disease or pneumonia requiring hospitalization during the 2002-03 winter/spring period in Québec City, Canada. In children, the detection rate for influenza A, influenza B, hRSV, and hMPV was 9/248 (3.6%), 4/248 (1.6%), 123/248 (49.6%), and 13/248 (5.2%), respectively. Five (2.0%) of the 248 children had a mixed viral infection. None of the NPA samples was found to contain PCR-inhibitory substances as shown by successful amplification of the internal control in all negative samples. In adults, the detection rate for influenza A, influenza B, hRSV, and hMPV was 3/108 (2.8%), 0/108 (0%), 13/108 (12.0%), and

2/108 (1.8%), respectively. One patient had a mixed viral infection (influenza A and hMPV). No samples contained PCR-inhibitory samples.

Example 11: Description and evaluation of the multiplex respiratory-2 PCR.

5

Same as example 9, except that the multiplex PCR assay is composed of the following PCR primers for detection of parainfluenza-1 (SEQ. ID. Nos. 147 and 148), parainfluenza-3 (SEQ. ID. Nos. 151 and 152), human adenoviruses (SEQ. ID. Nos. 153 and 155), and rhinoviruses/enteroviruses (SEQ. ID. Nos. 160 and 161). Primers are added in the PCR reaction mixture at a concentration of 0.2 μ M (SEQ. ID. Nos. 147 and 151), 0.3 μ M (SEQ. ID. Nos. 153 and 155), 0.4 μ M (SEQ. ID. Nos. 148 and 152), and 0.5 μ M (SEQ. ID. Nos. 160 and 161). The cycling conditions included an amplification step of 50 cycles of 15 s at 94°C, 5 s at 58°C, and 26 s at 72°C. The T_m values determined with the LightCycler instrument were 91.0°C, 80.0°C, 77.5°C, 89.0°C, 82.0°C, and 85.0°C for the internal control, parainfluenza-1, parainfluenza-3, adenoviruses, rhinoviruses, and enteroviruses, respectively (Fig. 8). The lower limit of detection of the multiplex respiratory-2 PCR was 50, 100, 10, 50, and 200 copies for parainfluenza-1, parainfluenza-3, adenoviruses, rhinoviruses, and enteroviruses, respectively, in the presence of 500 copies of an internal control (plasmid flanked by rhinovirus/enterovirus complementary primer sequences). The multiplex respiratory-2 assay was found to be specific with no amplification of influenza A, influenza B, hRSV, hMPV, coronavirus, herpes simplex virus type 1 and 2, varicella-zoster virus, cytomegalovirus, HHV-6, HHV-8, and Epstein-Barr virus.

25

Example 12 : Description of real-time PCR assays for the SARS-coronavirus.

30

Same as example 9, except that the PCR assay is composed uniquely of primers (two different possible sets) for the SARS-coronavirus as defined in SEQ. ID. Nos. 156-157 and 158-159. The concentration of the primers in the PCR reaction mixture is 0.5 μ M. The amplification step included 50 cycles of 15 s at 94°C, 5 s at 58°C, and 20 s at 72°C. The T_m for both PCR products is 83°C (Fig. 12).

Table 1: List of hMPV sequences revealed in the present invention

SEQ ID NO.	Isolate No.	Target gene
2	hMPV-118	Nucleoprotein
3	hMPV-174	Nucleoprotein
4	hMPV-176	Nucleoprotein
5	hMPV-193	Nucleoprotein
6	C-77807	Nucleoprotein
7	C-77748	Nucleoprotein
8	hMPV-217	Nucleoprotein
10	hMPV-163	Nucleoprotein
11	hMPV-174	Nucleoprotein
12	hMPV-184	Nucleoprotein
13	hMPV-185	Nucleoprotein
14	C-76837	Nucleoprotein
15	C-77807	Nucleoprotein
16	C-78123	Nucleoprotein
17	C-78132	Nucleoprotein
18	C-78163	Nucleoprotein
19	C-91205	Nucleoprotein
20	C-91364	Nucleoprotein
21	C-91830	Nucleoprotein
22	hMPV-Q86	Nucleoprotein
23	hMPV-Q97	Nucleoprotein
24	Can 97-83	Nucleoprotein
25	Can 98-75	Nucleoprotein
26	Can 98-75	Fusion type II
27	C-67345	Fusion type I
28	Can 97-83	Fusion type I
29	C-68661	Fusion type I
30	C-73750	Fusion type I
31	C-74549	Fusion type I
32	C-74783	Fusion type I
33	C-76837	Fusion type I
34	C-77748	Fusion type I
35	C-77807	Fusion type I
36	C-78132	Fusion type I
37	C-78163	Fusion type I
38	C-78406	Fusion type I
39	hMPV-174	Fusion type II
40	hMPV-193	Fusion type I
41	hMPV-194	Fusion type I
42	hMPV-198	Fusion type I
43	hMPV-217	Fusion type II
44	hMPV-208	Fusion type I
45	hMPV-223	Fusion type I
46	hMPV-228	Fusion type I

47	C-85885	Fusion type I
48	C-60298	Fusion type I
49	C-63778	Fusion type II
50	C-64199	Fusion type II
51	C-64200	Fusion type II
52	C-64536	Fusion type II
53	C-73769	Fusion type II
54	C-74501	Fusion type II
55	C-78429	Fusion type II
56	C-78562	Fusion type II
57	hMPV-118	Fusion type II
58	hMPV-200	Fusion type I
59	hMPV-176	Fusion type I
60	hMPV-193	Glycoprotein
61	hMPV-228	Glycoprotein
62	C-77748	Glycoprotein
63	C-78132	Glycoprotein
64	C-78406	Glycoprotein
65	C-73750	Glycoprotein
66	C-60298	Glycoprotein
67	C-74783	Glycoprotein
68	C-74549	Glycoprotein
69	C-77807	Glycoprotein
70	C-78163	Glycoprotein
71	C-68661	Glycoprotein
72	C-88448	Glycoprotein
73	C-88470	Glycoprotein
74	C-86316	Glycoprotein
76	hMPV-118	Polymerase
77	hMPV-163	Polymerase
78	hMPV-174	Polymerase
79	hMPV-184	Polymerase
80	hMPV-196	Polymerase
81	C-76837	Polymerase
82	C-77807	Polymerase
83	hMPV-185	Polymerase
84	C-78123	Polymerase
85	C-91205	Polymerase
86	C-91364	Polymerase
87	C-91749	Polymerase
88	hMPV-Q86	Polymerase
89	hMPV-Q97	Polymerase
90	Can 97-83	Polymerase

Table 2: List of hMPV PCR primers developed in the present invention

SEQ ID NO.	Target gene	Originating DNA	
		Position ^a	SEQ ID NO.
91	Nucleoprotein (N)	25	1
92	Nucleoprotein (N)	97	1
93	Nucleoprotein (N)	146 ^b	1
94	Nucleoprotein (N)	1025 ^b	1
95	Nucleoprotein (N)	58	9
96	Nucleoprotein (N)	986 ^b	9
97	Fusion (F)	3052	1
98	Fusion (F)	3810 ^b	1
99	Fusion (F)	4671 ^b	1
100	Matrix (M)	2165	1
101	Matrix (M)	2943 ^b	1
102	Phosphoprotein (P)	1248	1
103	Phosphoprotein (P)	2124 ^b	1
104	Glycoprotein (G)	6231	1
105	Glycoprotein (G)	6247	1
106	Glycoprotein (G)	6957 ^b	1
107	Glycoprotein (G)	6981 ^b	1
108	Glycoprotein (G)	6235	1
109	Glycoprotein (G)	7227 ^b	1
110	RNA polymerase (L)	142	75
111	RNA polymerase (L)	691 ^b	75
112	RNA polymerase (L)	7308	1
113	RNA polymerase (L)	7857 ^b	1
114	RNA polymerase (L)	7616	1

^a Position refers to nucleotide position of 5' end of primer. Oligonucleotides are 17-20 bp in length.

^b Primer is reverse-complement of target sequence.

Table 3: List of hMPV probes developed in the present invention

SEQ ID NO.	Target gene	Originating DNA	
		Position ^a	SEQ ID NO.
115	Nucleoprotein (N)	786	1
116	Nucleoprotein (N)	808	1
117	Fusion (F)	3163	1
118	Fusion (F)	3187	1
119	Matrix (M)	2636	1
120	Matrix (M)	2659	1
121	Phosphoprotein (P)	1492	1
122	Phosphoprotein (P)	1518	1
123	Glycoprotein (G)	6509	1
124	Glycoprotein (G)	6530	1
125	RNA polymerase (L)	7600	1
126	RNA polymerase (L)	7627	1
127	RNA polymerase (L)	7331	1
128	Nucleoprotein (N)	824	9
129	RNA polymerase (L)	434	75

^a Position refers to nucleotide position of 5' end of probe. Oligonucleotides are 21-25 bp in length.

Table 4: Length of amplicons obtained with different hMPV primer pairs which are objects of the present invention

SEQ ID NO.	Target Gene	Length of amplicon
91 + 94	Nucleoprotein (N)	1001 bp
92 + 94	Nucleoprotein (N)	929 bp
91 + 93	Nucleoprotein (N)	122 bp
97 + 99	Fusion (F)	1620 bp
97 + 98	Fusion (F)	759 bp
100 + 101	Matrix (M)	779 bp
102 + 103	Phosphoprotein (P)	877 bp
104 + 107	Glycoprotein (G)	751 bp
105 + 106	Glycoprotein (G)	711 bp
108 + 109	Glycoprotein (G)	993 bp
112 + 113	RNA polymerase (L)	550 bp
112+114	RNA polymerase (L)	308 bp

Table 5: Comparative evaluation of different hMPV primers for detection of hMPV strains

Strains No.	Type of sample	Year	N Primers		M primers		F primers		P primers		L primers	
			SEQ. ID. Nos. 92+94		SEQ. ID. Nos. 100+101		SEQ. ID. Nos. 97+98		SEQ. ID. Nos. 102+103		SEQ. ID. Nos. 112+113	
	I or S		+/-	Tm (°C)	+/-	Tm (°C)	+/-	Tm (°C)	+/-	Tm (°C)	+/-	Tm (°C)
C-74501	I	2000	+	82.92	-		+	83.65	-		+	78.14
C-74783	I	2000	+	82.76	+	83.49	-		+	81.51	+	78.20
C-76837	I	2000	+	82.94	+	83.43	+	83.17	+	80.86	-	
C-77719	I	2001	+	83.26	+	84.64	-		-		+	77.87
C-77738	I	2001	+	82.99	-		-		-		+	77.51
C-77748	I	2001	+	83.06	+	82.96	+	83.10	+	81.27	+	77.38
C-77807	I	2001	+	82.99	+	83.26	+	83.25	+	80.65	+	78.34
C-78024	I	2001	+	82.86	+	83.95	-		-		-	
C-78028	I	2001	+	82.98	+	83.13	-		-		+	78.32
C-78123	I	2001	+	82.83	-		-		-		+	78.48
C-85984	I	2002	+	82.59	+	83.21	+	83.51	+	79.99	+	77.97
C-85448	I	2002	+	83.66	+	82.72	-		+	80.31	+	78.88
C-85983	I	2002	+	82.59	+	83.03	+	83.88	+	80.46	+	78.01
C-85988	I	2002	+	82.17	-		+	84.39	-		+	78.06
C-86316	I	2002	+	82.64	+	82.75	+	83.18	+	80.18	+	78.02
C-85126	I	2002	+	81.89	+	82.05	+	82.39	+	80.00	+	78.04
C-85473	I	2002	+	82.39	+	82.57	+	82.91	+	80.74	+	77.82
C-85332	I	2002	+	81.98	-		-		-		+	77.72
C-85596	I	2002	+	82.24	+	82.73	+	83.17	+	80.35	+	77.58
C-85542	I	2002	+	82.22	+	82.72	-		+	80.08	+	77.67
HMPV-118	S	2002	+	82.47	-		-		-		ND	ND
HMPV-174	S	2002	+	82.18	+	82.06	+	83.16	+	80.17	+	78.20
HMPV-176	S	2002	+	81.41	-		+	83.97	-		+	77.81
HMPV-193	S	2002	+	82.22	+	81.89	+	83.00	+	80.58	+	77.94
HMPV-194	S	2002	+	82.24	+	81.32	+	82.98	-		+	77.84
HMPV-198	S	2002	+	82.66	-		-		-		-	
HMPV-200	S	2002	+	82.53	-		+	83.46	-		+	77.62
HMPV-208	S	2002	+	82.11	+	81.81	+	83.33	+	80.06	+	78.40
HMPV-217	S	2002	+	82.13	+	81.58	+	83.01	-		+	77.76

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HMPV-	S	2002	+	81.89	+	82.36	+	83.04	-	+	78.10
223											
Mean				82.63 ± 0.87		82.75 ± 0.80		83.29 ± 0.45		80.48 ± 0.46	77.99 ± 0.33

Note: I = viral isolates; S = clinical specimens; Tm = melting temperature as determined by a LightCycler instrument.

Table 6: Size of the viral fusion (F) gene fragments obtained for different hMPV isolates following enzymatic digestion with restriction endonucleases

SEQ ID NO.	Fragments obtained after digestion with the restriction endonuclease		F genotype ^a
	ApaI	Avr II	
35	532 bp + 227 bp	759 bp	I
58	532 bp + 227 bp	759 bp	I
39	759 bp	447 bp + 312 bp	II
40	532 bp + 227 bp	759 bp	I
41	532 bp + 227 bp	759 bp	I
43	759 bp	447 bp + 312 bp	II
44	532 bp + 227 bp	759 bp	I
59	532 bp + 227 bp	759 bp	I
45	532 bp + 227 bp	759 bp	I

5 ^aAs determined by DNA sequencing and phylogenetic studies.

Table 7. Type of laboratory confirmation by type of infection

Laboratory test	hMPV		hRSV		Influenza A		Adenovirus		PIV 2	
	Tests	Positive	Tests	Positive	Tests	Positive	Tests	Positive	Tests	Positive
	done		Done		done		done		done	
PCR	208	12 5.8%	208	106 51.0%	208	45 21.6%	NA	NA	NA	NA
Culture	100	2 2%	100	31 31%	100	14 14%		6 6%	100	1 1%
Antigen detection (Immunofluorescence)	NA	NA	NA	NA	NA	NA	81	1 1%	76	1 1.3%
Antigen detection (ELISA)	NA	NA	204	94 46.1%	100	14 14%	NA	NA	NA	NA
Total (+) in at least one test	12 (5.8%)		118 (56.7%)		49 (23.6%)		6 (6%)		2 (2%)	

Delay between onset of symptoms and NPA, days					
Mean/median	6.3/5.0	5.2/4.0	8.7/5.0	6.0/6.5	3.0/3.0
Note: hMPV, human metapneumovirus; hRSV, human respiratory syncytial virus; PTV, parainfluenza virus; NPA, nasopharyngeal aspirate; NA, not available.					

Table 8. Signs and symptoms by type of viral infection

Signs and symptoms	EMPV	hRSV	Influenza A	Single virus	Multiple viruses	No virus detected	Total
	N=12	N=118	N=49	N=141	N=23	N=44	N=208
Fever	8	67	38	85	17	25	127
	67%	57%	78%	60%	74%	57%	61%
Cough	12	117	47	138	23	40	201
	100%	99%	96%	98%	100%	90%	97%
Rhinorrhea	11	107	41	123	22	42	187
	92%	91%	84%	87%	96%	96%	90%
Retractions	11	112	40	125	22	39	186
	92%	95%	82%	89%	96%	89%	89%
Wheezing	10	77	28	83	19	31	133
	83%	65%	57%	59%	83%	71%	64%
Lacrymation	3	37	15	46	6	11	63
	25%	31%	31%	33%	26%	25%	30%
Diarrhea	1	19	13	24	5	10	39

	8%	17%	27%	17%	22%	23%	19%
Vomiting	3	9	5	10	4	1	15
	25%	8%	10%	7%	17%	2%	7%
Other	0	31	9	33	4	9	46
		26%	18%	23%	17%	21%	22%

Note: hMPV, human metapneumovirus; hRSV, human respiratory syncytial virus.

Table 9. Final diagnoses (complications) by type of viral infection

Complications	hMPV N = 12	HRSV N = 118	Influenza A N = 49	Single virus N = 141	Multiple viruses N = 23	No virus detected N = 44	Total N = 208
Bronchiolitis	8 66.7%	99 83.9%	25 51.0%	98 69.5%	19 82.6%	25 56.8%	142 68.3%
Otitis	6 50.0%	70 59.3%	27 55.1%	78 55.3%	15 65.2%	24 54.6%	117 56.3%
Pneumonia	2 16.7%	30 25.4%	18 36.7%	39 27.7%	7 30.4%	12 27.3%	58 27.9%
Laryngotracheobronchitis	0	10 8.5%	6 12.2%	9 6.4%	4 17.4%	1 2.3%	14 6.7%
Sinusitis	0	3 2.5%	3 6.1%	2 1.4%	2 8.7%	1 2.3%	5 2.4%
Pharyngitis	0	1 0.9%	0	2 1.4%	0	2 4.6%	4 1.9%
Flu syndrome	0	2 1.7%	0	2 1.4%	0	4 9.1%	6 2.9%

Croup	0	2	0	2	0	1	3
		1.7%		1.4%		2.3%	1.4%
Other	1	4	3	9	0	5	14
	8.3%	3.4%	6.1%	6.4%		11.4%	6.7%

Note: hMPV, human metapneumovirus; hRSV, human respiratory syncytial virus.

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Table 10: List of PCR primers used for amplification of respiratory viruses

Primer SEQ ID NO.	Virus	Target Gene	Originating DNA Position ^a	SEQ ID NO.
139	Influenza A	Matrix	32 / 7	130-131
140	Influenza A	Matrix	276 ^b / 251 ^b	130-131
141	Influenza B	Matrix	82	132
142	Influenza B	Matrix	605 ^b	132
143	RSV	Fusion	1111	133
144	RSV	Fusion	1490 ^b	133
95	hMPV	Nucleocapsid	58	9
96	hMPV	Nucleocapsid	986 ^b	9
110	hMPV	Polymerase	142	75
111	hMPV	Polymerase	691 ^b	75
145	PIV-1	Nucleocapsid	64	134
146	PIV-1	Nucleocapsid	147 ^b	134
149	PIV-3	Nucleocapsid	416	135
150	PIV-3	Nucleocapsid	649 ^b	135
154	Adenovirus	Hexon	154	136
155	Adenovirus	Hexon	368 ^b	136
160	Enterovirus	5'-non coding region	94 / 71	137/138
161	Enterovirus	5'-non coding region / VP2	746 ^b / 603 ^b	137/138
141	IC ^c multiplex 1	DNA polymerase HSV-2	1	170
142	IC ^c multiplex 1	DNA polymerase HSV-2	558 ^b	170
160	IC ^c multiplex 2	DNA polymerase HSV-2	1	171
161	IC ^c multiplex 2	DNA polymerase HSV-2	554 ^b	171
112	hMPV	Polymerase	7308	1
114	hMPV	Polymerase	7616	1
147	PIV-1	Nucleocapsid	822	134
148	PIV-1	Nucleocapsid	1029	134
151	PIV-3	Nucleocapsid	792	135
152	PIV-3	Nucleocapsid	902	135
153	Adenovirus	Hexon	7	136
156	Sars-CoV	nsp9		
157	Sars-CoV	nsp9		
158	Sars-CoV	nsp11		
159	Sars-CoV	nsp11		

^a Position refers to nucleotide position of 5'-end of primer. Oligonucleotides are 16-26 bp in length.

^b Primer is reverse-complement of target sequence.

^c IC refers to the internal control used to monitor the efficiency of the PCR amplification

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Table 11: List of viral probes developed in the present invention

Probe SEQ ID NO.	Target	Originating DNA	
		Position ^a	SEQ ID NO.
162	Influenza A	114 ^b / 89 ^b	130/131
163	Influenza B	383	132
164	hRSV	1391 ^b	133
128	hMPV	824	9
129	hMPV	434	75
165	PIV-1	96	134
166	PIV- 3	616 ^b	135
167	Adenovirus	223	136
168	Rhinovirus	467 ^b	138
169	Enterovirus	644 ^b	137
172	Internal Control ^c	321 ^b / 325 ^b	170/171

^aPosition refers to nucleotide position of 5'-end of primer. Oligonucleotides are 20-23 bp in length.

^bProbe is reverse-complement of target sequence.

^cA modified DNA polymerase gene sequence of herpes simplex virus (HSV) type 2 serves as the internal control template.

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Table 12: Length of amplicons obtained with the different viral primer pairs

Primer SEQ ID NO.	Virus	Target gene	Length of amplicons
139 + 140	Influenza A	Matrix	245 bp
141 + 142	Influenza B	Matrix	524 bp
143 + 144	hRSV	Fusion	380 bp
95 + 96	hMPV	Nucleocapsid	929 bp
110 + 111	hMPV	Polymerase	550 bp
145 + 146	PIV-1	Nucleocapsid	84 bp
149 + 150	PIV-3	Nucleocapsid	234 bp
154 + 155	Adenoviruses	Hexon	215 bp
160 + 161	Rhinoviruses	5'-non coding region - VP2	533 bp
160 + 161	Enteroviruses	5'-non coding region	653 bp
141 + 142	IC multiplex 1	DNA polymerase HSV-2	558 bp
160 + 161	IC multiplex 2	DNA polymerase HSV-2	554 bp
112 + 114	hMPV	Polymerase	308 bp
147 + 148	PIV-1	Nucleocapsid	208 bp
151 + 152	PIV-3	Nucleocapsid	111 bp
153 + 155	Adenovirus	Hexon	362 bp
156 + 157	Sars-CoV	nsp9	198 bp
158 + 159	Sars-CoV	nsp11	368 bp

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Table 13: Selection of primer sets with resulting melting temperature (T_m) values of the corresponding amplicons for each multiplex assay

Primer SEQ ID NO.	Target	Multiplex NO.	T _m (°C)
139 + 140	Influenza A	1	85
141 + 142	Influenza B	1	83
143 + 144	hRSV	1	79
95 + 96 or 112 + 114	hMPV	1	82 or 77
141 + 142	Internal Control	1	91
147 + 148	Parainfluenza 1	2	80.0
151 + 152	Parainfluenza 3	2	77.5
153 + 155	Adenovirus	2	89.0
160 + 161	Rhinovirus	2	82.0
160 + 161	Enterovirus	2	85.0
160 + 161	Internal Control	2	91

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Table 14. Evaluation of the multiplex PCR respiratory assay with temporally-different strains of influenza (Flu) and human respiratory syncytial (HRSV) viruses.

Virus	Subtype / Genotype ^a	Year	Type	Strain	T _m (°C)
Flu A	H1	99-00	clinical	-	85.10
Flu A	H1	99-00	clinical	-	85.39
Flu A	H1	00-01	clinical	-	85.12
Flu A	H1	00-01	clinical	-	85.20
Flu A	H1	00-01	clinical	-	85.04
Flu A	H1	01-02	clinical	-	84.62
Flu A	H1	01-02	clinical	-	85.07
Flu A	H1	02-03	clinical	-	85.50
Flu A	H1	02-03	clinical	-	85.29
Flu A	H1	95	vaccine	A/Beijing/262/95	85.06
Flu A	H1	33	vaccine	A/WSN/33	85.25
Mean AH1					85.15±0.22
Flu A	H3	98-99	clinical	-	85.58
Flu A	H3	98-99	clinical	-	85.18
Flu A	H3	98-99	clinical	-	85.35
Flu A	H3	98-99	clinical	-	85.57
Flu A	H3	98-99	clinical	-	85.37
Flu A	H3	01-02	clinical	-	85.07
Flu A	H3	01-02	clinical	-	85.65
Flu A	H3	02-03	clinical	-	84.92
Flu A	H3	99	vaccine	A/Panama/2007/99	85.18
Flu A	H3	97	vaccine	A/Sydney/5/97	85.06
Mean AH3					85.31±0.25
Mean FluA					85.27±0.22
Flu B	-	98-99	clinical	-	83.87
Flu B	-	98-99	clinical	-	83.12
Flu B	-	00-01	clinical	-	83.01
Flu B	-	00-01	clinical	-	83.03
Flu B	-	00-01	clinical	-	82.88
Flu B	-	00-01	clinical	-	83.75
Flu B	-	00-01	clinical	-	83.17
Flu B	-	02-03	clinical	-	83.89
Flu B	-	02-03	clinical	-	83.84
Flu B	-	97	vaccine	B/Harbin/7/97	84.12
Mean FluB					83.47±0.46

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Table 14. Evaluation of the multiplex PCR respiratory assay with temporally-different strains of influenza (Flu) and human respiratory syncytial (HRSV) viruses. (Continued).

HRSV	B	99-00	clinical	-	79.32
HRSV	A	99-00	clinical	-	79.83
HRSV	A	00-01	clinical	-	79.06
HRSV	A	00-01	clinical	-	78.85
HRSV	B	01-02	clinical	-	79.34
HRSV	B	01-02	clinical	-	79.52
HRSV	B	01-02	clinical	-	79.98
HRSV	B	01-02	clinical	-	79.52
HRSV	A	01-02	clinical	-	79.84
HRSV	B	01-02	clinical	-	79.42
HRSV	B	01-02	clinical	-	79.49
HRSV	B	01-02	clinical	-	79.48
HRSV	B	01-02	clinical	-	79.55
HRSV	B	01-02	clinical	-	79.32
HRSV	A	01-02	clinical	-	79.77
HRSV	A	01-02	clinical	-	79.92
HRSV	A	01-02	clinical	-	79.40
Mean HRSV-A					79.52±0.43
Mean HRSV-B					79.49±0.19
Mean HRSV					79.51±0.30

^a Subtyping was performed by multiplex PCR for the influenza hemagglutinin gene (2) whereas genotyping was done by conventional PCR for the HRSV G gene (22)

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Table 15. Evaluation of the multiplex PCR respiratory assay for detection of influenza A (Flu A) virus.

		Antigenic test (Directigen Flu A+B) (n = 172)		Flu A M2 PCR assay ^a (n = 27)	
		+	-	+	-
Multiplex PCR	+	17	25	22	3
	-	2	128	0	2

5 Sensitivity: $39/39 = 100\%$
 Specificity: $130/133 = 97.7\%$
 Positive predictive value: $39/42 = 92.8\%$
 Negative predictive value: $130/130 = 100\%$

10 ^a Only performed for samples showing discordant results with the
 multiplex PCR assay and the antigenic test.

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Table 16: Evaluation of discordant test results for influenza A (Flu A) virus.

Sample No.	Multiplex PCR Flu A results (C _T) ^a	Antigenic test Flu A results	M2 PCR Flu A results	Other PCR- amplified viruses ^b
16	-	+	-	HRSV
23	+(27)	-	+	
24	-	+	-	HRSV
27	+(28)	-	+	HRSV
35	+(28)	-	+	HRSV
36	+(32)	-	+	
40	+(34)	-	+	
43	+(36)	-	+	HRSV
44	+(35)	-	+	
50	+(34)	-	+	
51	+(33)	-	+	HRSV
103	+(35)	-	+	
107	+(35)	-	+	
114	+(37)	-	-	
118	+(38)	-	+	HRSV
120	+(36)	-	+	HRSV
125	+(38)	-	+	
130	+(35)	-	+	HRSV
131	+(36)	-	-	
132	+(24)	-	+	HRSV
134	+(36)	-	-	
141	+(28)	-	+	
152	+(34)	-	+	
158	+(32)	-	+	
160	+(33)	-	+	HRSV
161	+(28)	-	+	HRSV
163	+(32)	-	+	

^a Cycle threshold value as determined by LightCycler.^b Viruses amplified by the multiplex PCR assay i. e. influenza (Flu) A and B as well as the human respiratory syncytial virus (HRSV).

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Table 17: Evaluation of the multiplex PCR respiratory assay for detection of human respiratory syncytial virus (HRSV).

		Antigenic test (RSV TestPack) (n = 204)		HRSV gG PCR assays ^a (n = 32)	
		+	-	+	-
Multiplex PCR	+	83	21	20	1
	-	11	89	6	5

5 Sensitivity: $103/109 = 94.5\%$
 Specificity: $94/95 = 98.9\%$
 Positive predictive value: $103/104 = 99.0\%$
 Negative predictive value: $94/100 = 94.0\%$

10 ^a Only performed for samples showing discordant results with the multiplex PCR assay and the antigenic test.

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Table 18: Evaluation of discordant test results for human respiratory syncytial virus (HRSV).

Sample No.	Multiplex PCR HRSV results (C _T) ^a	Antigenic test HRSV results	Glycoprotein G PCR HRSV results (genotype)	Other PCR- amplified viruses ^b
16	+(32)	-	+(B)	
17	+(27)	-	+(B)	
26	+(36)	-	+(B)	
34	-	+	-	
35	+(33)	-	+(B)	Flu A
43	+(36)	-	+(A)	Flu A
46	+(34)	-	+(B)	
55	+(34)	-	+(B)	
58	+(33)	-	+(B)	
62	-	+	+(A)	Flu A
70	+(37)	-	+(B)	
71	+(35)	-	+(B)	
72	+(34)	-	+(B)	
73	+(26)	-	+(A)	
79	+(33)	-	+(B)	
80	-	+	-	
91	+(35)	-	+(A)	
95	+(29)	-	+(B)	
100	+(30)	-	+(A)	
112	-	+	-	
129	+(34)	-	+(B)	
130	+(35)	-	+(B)	Flu A
134	-	+	+(A)	Flu A
139	-	+	+(A)	
142	-	+	+(A)	Flu A
144	-	+	+(B)	Flu A
150	+(34)	-	-	
187	+(31)	-	+(A)	
191	+(29)	-	+(A)	

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Table 18: Evaluation of discordant test results for human respiratory syncytial virus (HRSV). (Continued).

193	-	+	+(A)
211	-	+	-
212	-	+	-

5

^a Cycle threshold value as determined by Lightcycler.

^b Viruses amplified by the multiplex PCR assay i. e. influenza (Flu) A and B as well as the human respiratory syncytial virus (HRSV).

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CLAIMS:

- 1- A method for detecting and/or quantifying human metapneumovirus (hMPV) in a sample said method comprising:
- 5 -providing at least one probe or primer specific for a nucleic acid sequence of said hMPV;
- contacting said at least one probe and/or primer with said sample to allow annealing of said probe and/or primer with said nucleic acid sequence; and
- detecting and/or quantifying said nucleic acid sequence using said annealed probe and/or primer.
- 10 2- The method as claimed in claim 1 wherein said nucleic acid sequence is comprised in a hMPV gene selected from a group consisting of nucleocapsid (N), phosphoprotein (P), matrix (M), fusion (F), membrane (M2), polymerase (L), glycoprotein (G) and small hydrophobic (SH) genes.
- 15 3- The method as claimed in claim 2 wherein said nucleic acid sequence is selected from any one of SEQ ID NO 2-8, 10-74, 76-90 or fragments thereof.
- 4- The method as claimed in claim 3 wherein said probe or primer is at least 10
- 20 nucleotides in length.
- 5- A method for detecting and/or quantifying human metapneumovirus (hMPV) in a sample said method comprising:
- 25 -performing reverse transcription using a template RNA derived from said sample to obtain a nucleic acid product;
- amplifying said nucleic acid product using a pair of oligonucleotide primers wherein said primers are specific for a sequence comprised in a hMPV gene selected from a group consisting of nucleocapsid (N), phosphoprotein (P), matrix (M), fusion

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(F), membrane (M2), polymerase (L), glycoprotein (G) and small hydrophobic (SH) genes to produce an amplification product; and

-detecting and/or quantifying said amplification product.

5 6- The method as claimed in claim 5 wherein said oligonucleotide primers are at least 10 nucleotides in length and capable of hybridizing with any one of SEQ ID 2-8, 10-74, 76-90.

7- The method as claimed in claim 5 or 6 wherein said step of performing reverse
10 transcription comprises contacting said template RNA with a primer selected from SEQ ID Nos 91-114 and wherein said oligonucleotide primers for PCR are selected from SEQ ID Nos 91-114.

8- The method as claimed in any one of claim 5-7 wherein said oligonucleotide
15 primers are pairs of primers selected from SEQ ID Nos 91 and 94, 92 and 94, 91 and 93, 97 and 99, 97 and 98, 100 and 101, 102 and 103, 104 and 107, 105 and 106, 108 and 109, 112 and 113 and 112 and 114.

9- The method as claimed in claim 5 wherein said template RNA is contacted
20 with primer selected from SEQ ID NO 91-94 and 112-114 and wherein said oligonucleotide primers are selected from SEQ ID NO 91-94 and 112-114.

10- The method as claimed in any one of claim 5-9 wherein said step of
25 amplifying is performed using PCR.

11- The method as claimed in claim 10 wherein said PCR is RT-PCR.

12- The method as claimed in claim 11 wherein said RT-PCR is real time RT-
30 PCR.

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- 13- The method as claimed in claim 11 or 12 wherein said RT-PCR comprises detecting said amplification products by characteristic melting temperature of said amplification products.
- 5 14- The method as claimed in claim 11 or 12 wherein said RT-PCR comprises detecting and/or quantifying said amplification products with probes specific for said products.
- 15- The method as claimed in claim 14 wherein said probes are selected from SEQ
10 ID no 115-129.
- 16- A composition for detecting a hMPV said composition comprising a combination of oligonucleotides for performing reverse transcription of a template RNA from said hMPV virus and for an amplification reaction of a product obtained
15 from said reverse transcription wherein said oligonucleotides for said amplification reaction are specific for a sequence comprised in a hMPV gene selected from a group consisting of nucleocapsid (N), phosphoprotein (P), matrix (M), fusion (F), membrane (M2), polymerase (L), glycoprotein (G) and small hydrophobic (SH) genes.
- 20 17- The composition of claim 16 wherein said oligonucleotides for said amplification reaction are primers selected from the group comprising SEQ ID Nos 91-114 and combination thereof.
- 18- A kit comprising a combination of oligonucleotides wherein the oligonucleotides
25 are selected from:
SEQ ID NOs: 91-114 and the pairs of SEQ ID Nos 91 and 94, 92 and 94, 91 and 93, 97 and 99, 97 and 98, 100 and 101, 102 and 103, 104 and 107, 105 and 106, 108 and 109, 112 and 113 and 112 and 114.
- 30 19- A method for typing an hMPV strain which comprises the steps of:

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-amplifying an hMPV nucleic acid fragment and detecting specific viral sequences;

-digesting said fragment with one or more restriction endonuclease; and

-analysing the restriction fragment length polymorphisms.

5

20- The method as claimed in claim 19 wherein said nucleotide sequences are found in fusion(F) or glycoprotein (G) gene.

10

21- The method as claimed in claim 20 wherein said sequences are selected from SEQ ID NO 26-74.

22- A method for detecting and/or quantifying two or more respiratory viruses in a sample said method comprising:

15 -providing at least two probes and/or primers specific for a nucleic acid sequences in said two or more respiratory viruses;

-contacting said at least two probes and/or primers with said sample to allow annealing of said probes and/or primers with said nucleic acid sequences; and

-detecting and/or quantifying said nucleic acid sequences using said annealed probes and/or primers.

20

23- The method as claimed in claim 22 wherein at least one of said nucleic acid sequences is comprised in a hMPV gene selected from a group consisting of nucleocapsid (N), phosphoprotein (P), matrix (M), fusion (F), membrane (M2), polymerase (L), glycoprotein (G) and small hydrophobic (SH) genes.

25

24- The method as claimed in claim 23 wherein said nucleic acid sequence is selected from any one of SEQ ID NO 2-8, 10-74, 76-90 or fragments thereof.

25- The method as claimed in claim 24 wherein said probes and/or primers are at
30 least 10 nucleotides in length.

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26- A method for detecting and/or quantifying two or more respiratory viruses in a sample said method comprising:

- 5 -performing reverse transcription using a template RNA derived from said sample to obtain nucleic acid products for each of said viruses;
 -amplifying said nucleic acid products using two or more pairs of oligonucleotide primers to produce an amplification product; and
 -detecting and/or quantifying said amplification products.

10

27- The method as claimed in claim 26 wherein at least one of said primers is specific for a sequence comprised in a hMPV gene selected from a group consisting of nucleocapsid (N), phosphoprotein (P), matrix (M), fusion (F), membrane (M2), polymerase (L), glycoprotein (G) and small hydrophobic (SH) genes.

15

28- The method as claimed in claim 27 wherein said oligonucleotide primers specific for a sequence comprised in a hMPV gene are capable of hybridizing with any one of SEQ ID 2-8, 10-74, 76-90.

20

29- The method as claimed in claim 28 wherein said oligonucleotide primers are at least 10 nucleotides in length.

30- The method as claimed in claim 29 wherein said oligonucleotide primer
25 specific for a sequence comprised in a hMPV gene are selected from SEQ ID Nos 91-114.

31- The method as claimed in any one of claim 26-30 wherein said at least two
30 respiratory viruses comprise influenza A and B, human respiratory syncytial viruses A and B, parainfluenza viruses (PIV) types 1-4, adenoviruses, rhinoviruses,

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enteroviruses and coronaviruses or any combination thereof and wherein said primers and said two or more viruses are selected such that the detection and or quantification is specific for each of said viruses.

5 32- The method as claimed in claim 31 wherein said oligonucleotide primers are at least 10 nucleotides in length and capable of hybridizing with any one of SEQ ID NO 130-138 and 170-171.

10 33- The method as claimed in claim 31 or 32 wherein said at least two viruses are influenza A, human Respiratory syncytial virus, human metapneumovirus and influenza B.

15 34- The method as claimed in claim 31 or 32 wherein said at least two viruses are Parainfluenza 1, Rhinovirus, Adenovirus, Parainfluenza 3, Enterovirus, and coronavirus.

20 35- The method as claimed in claim 31 wherein said pairs of oligonucleotide primers are selected from SEQ ID Nos 139 and 140, 141 and 142, 143 and 144, 92 and 94, 112 and 113, 112 and 114, 145 and 146, 147 and 148, 149 and 150, 151 and 152, 154 and 155, 153 and 155, 156 and 157, 158 and 159, 160 and 161.

25 36- The method as claimed in any one of claim 26-35 wherein said step of amplifying is performed using PCR and said primer are selected such that the products of the amplifications can be distinguished.

37- The method as claimed in claim 36 wherein said PCR is RT-PCR.

38- The method as claimed in claim 37 wherein said RT-PCR is real time RT-PCR.

30

- 89 -

39- The method as claimed in claim 37 or 38 wherein said RT-PCR comprises detecting said amplification products by characteristic melting temperature of said amplification products.

5 40- The method as claimed in claim 37 or 38 wherein said RT-PCR comprises detecting and/or quantifying said amplification products with probes specific for said products.

41- The method as claimed in claim 40 wherein said probes are selected from SEQ
10 ID no 162-169 and 172.

42- A composition for detecting at least two respiratory viruses said viruses comprising at least hMPV said composition comprising a combination of oligonucleotides for performing reverse transcription of a template RNA from said at
15 least two respiratory viruses and for an amplification reaction of a product obtained from said reverse transcription wherein said oligonucleotides for said amplification reaction comprise oligonucleotides specific for a sequence comprised in a hMPV gene selected from a group consisting of nucleocapsid (N), phosphoprotein (P), matrix (M), fusion (F), membrane (M2), polymerase (L), glycoprotein (G) and small hydrophobic
20 (SH) genes.

43- The composition of claim 42 wherein said oligonucleotides for said amplification reaction are primers selected from the group comprising SEQ ID Nos 91-114 and combination thereof.

25

44- A method for simultaneously detecting two or more respiratory tract viruses in a sample, said method comprising:

- 90 -

Selecting primers specific for a nucleic acid sequence in each of said two or more viruses, said primers to be used in an amplification reaction for detection of said nucleic acid sequences;

5 distributing said primers in one or more assay mixture comprising said sample and at least two pairs of primers; and

wherein said selecting and said distributing is based on said detection of said nucleic acid sequence of said two or more viruses being substantially free of overlap and
10 enabling to distinguish between said two or more viruses.

45- The method as claimed in claim 44 wherein said amplification reaction is PCR.

15

46- The method as claimed in claim 45 wherein said PCR is RT-PCR.

47- The method as claimed in claim 45 wherein said RT-PCR is real time RT-PCR.

20

48- The method as claimed in claim 24 wherein said detection is melting temperature.

49- An isolated nucleic acid comprising a sequence that hybridizes under stringent
25 conditions to a hybridization probe the nucleotide sequence of which consists of any one of SEQ ID NO 2-8, 10-74, 76-90 or complements thereof.

50- A kit comprising a nucleic acid probe that is at least 10 nucleotides in length and is selected from a group consisting sequences hybridizable to SEQ ID Nos 2-8, 10-74,
30 76-90 or fragments thereof.

- 91 -

51- A human metapneumovirus (hMPV) deposited with the International Depository Authority of Canada under Accession number IDAC 111203-01 (CAN97-83).

- 5 52- A human metapneumovirus (hMPV) deposited with the International Depository Authority of Canada under Accession number IDAC 111203-02 (CAN98-75).

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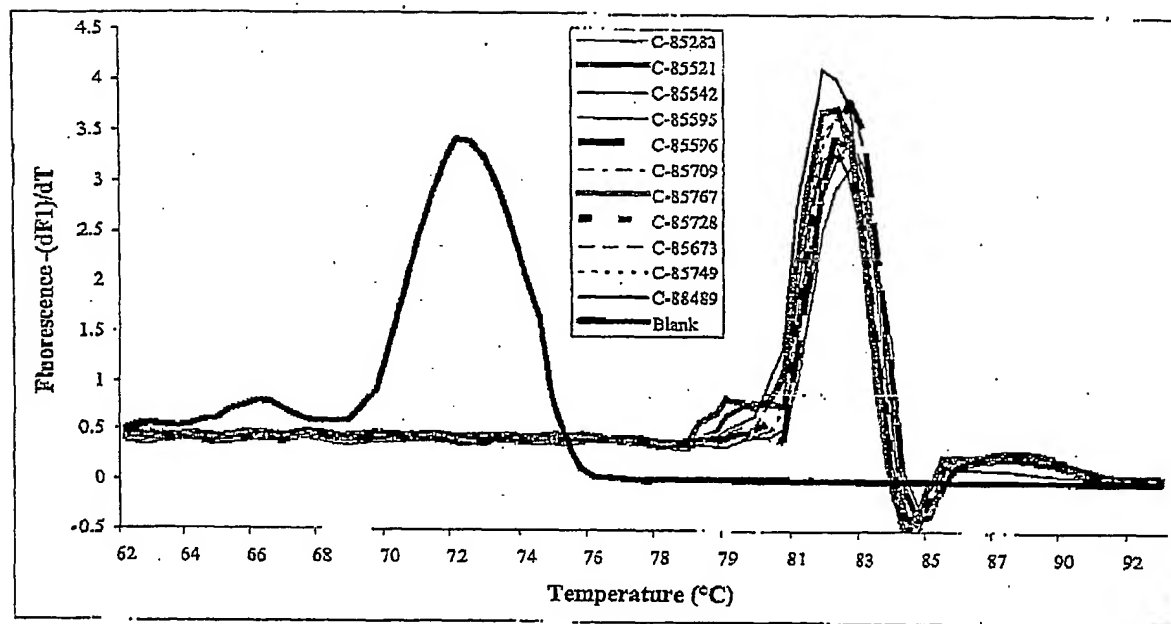


FIGURE 1

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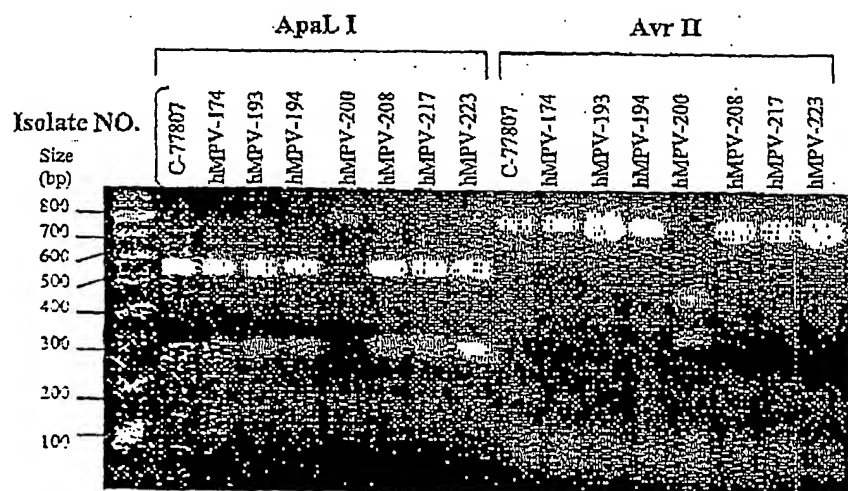


FIGURE 2

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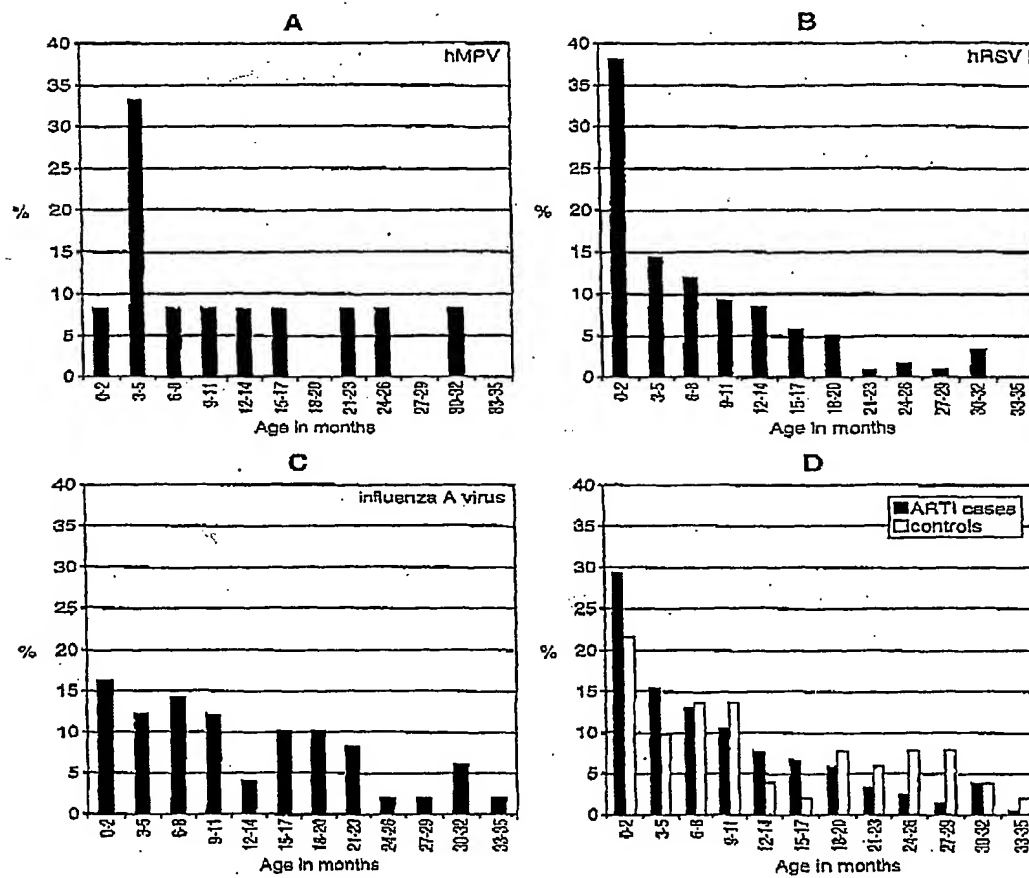


FIGURE 3

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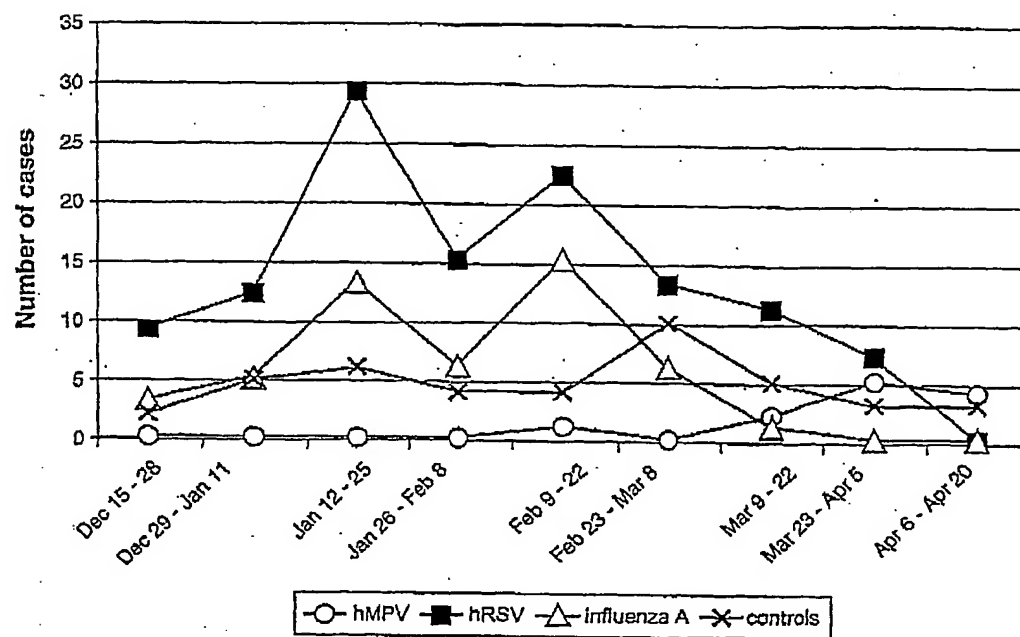


FIGURE 4

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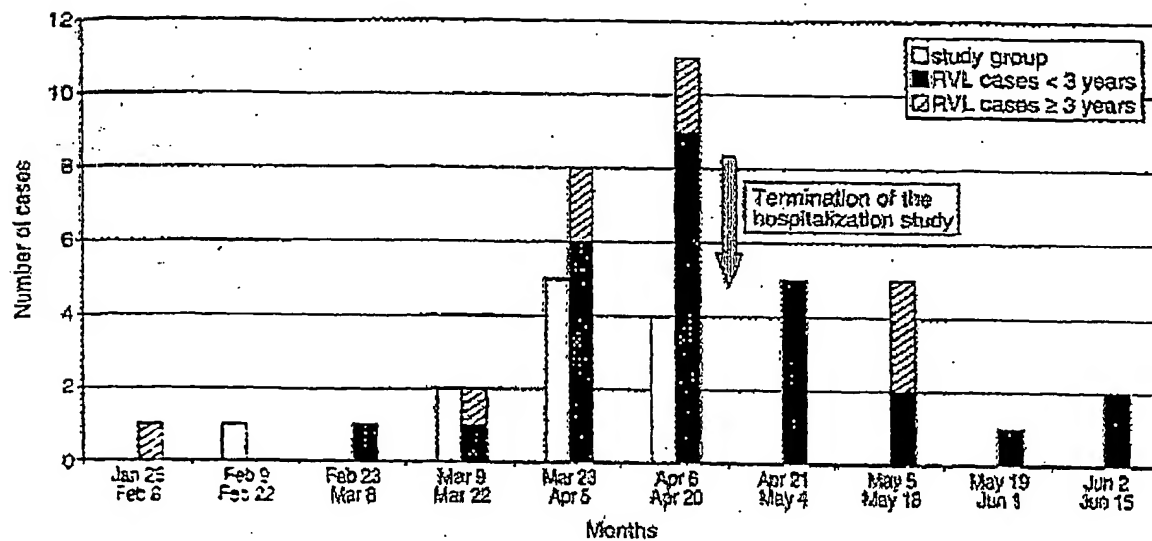


FIGURE 5

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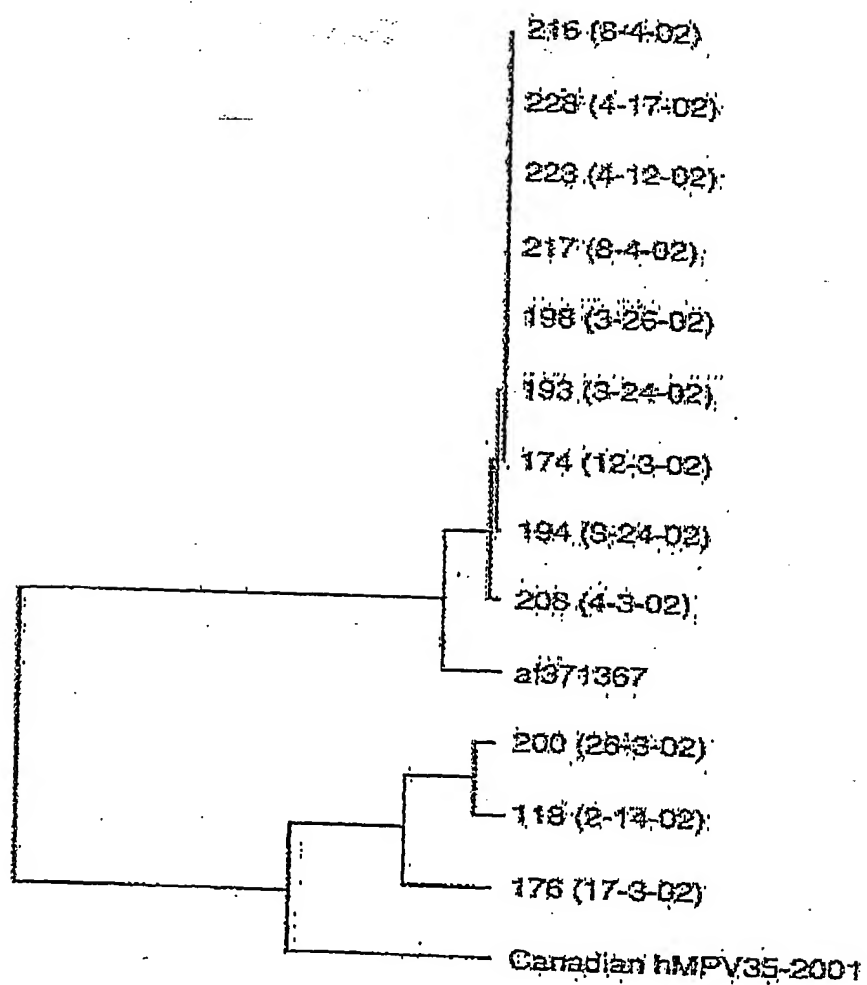


FIGURE 6

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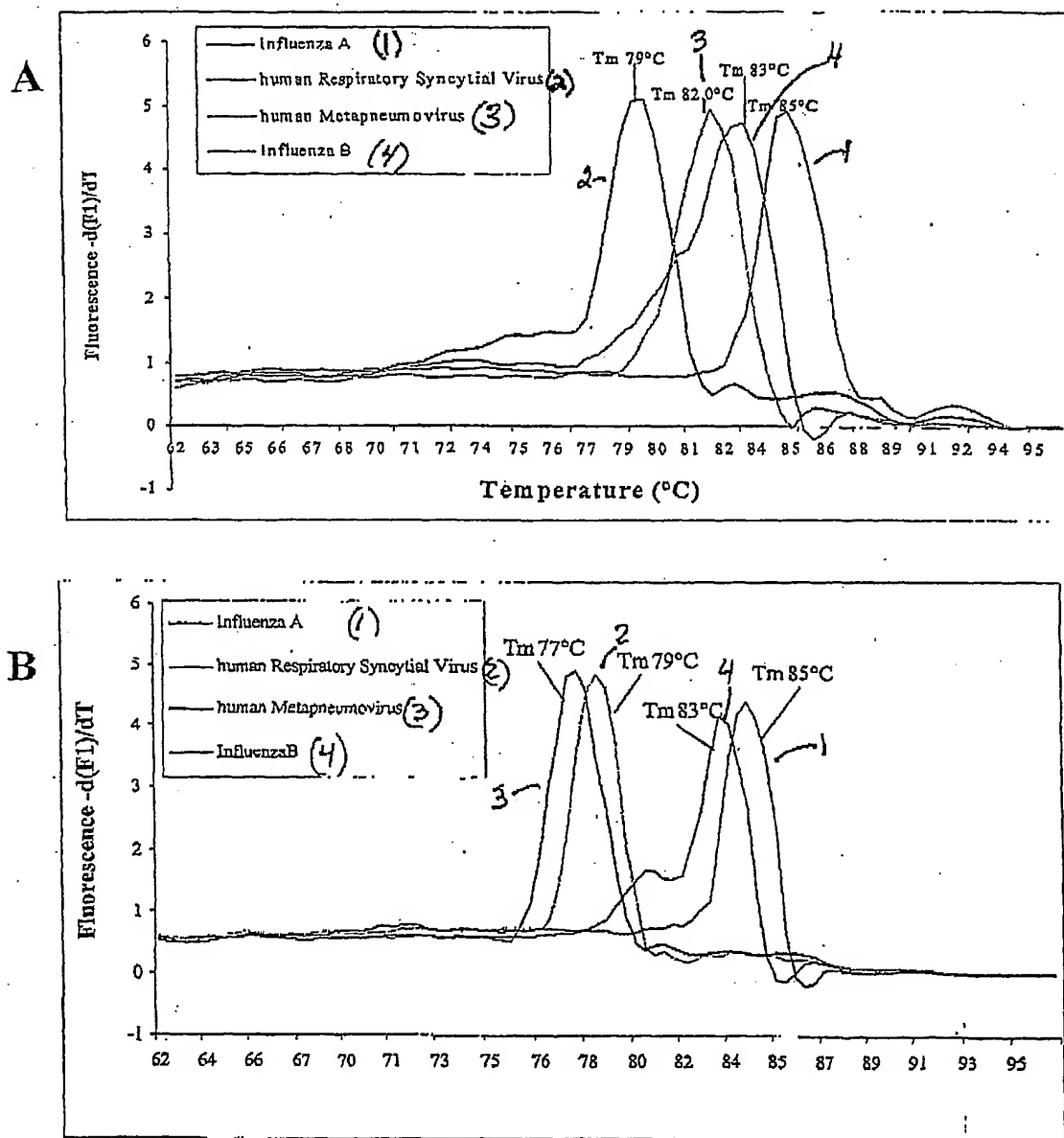


FIGURE 7

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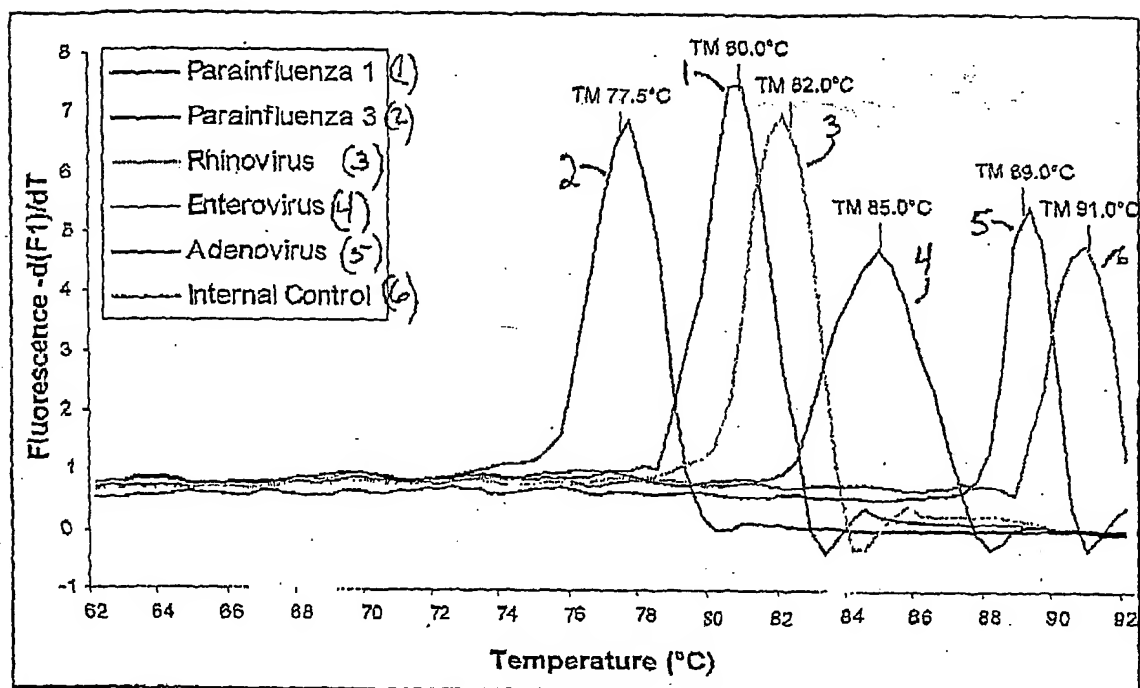


FIGURE 8

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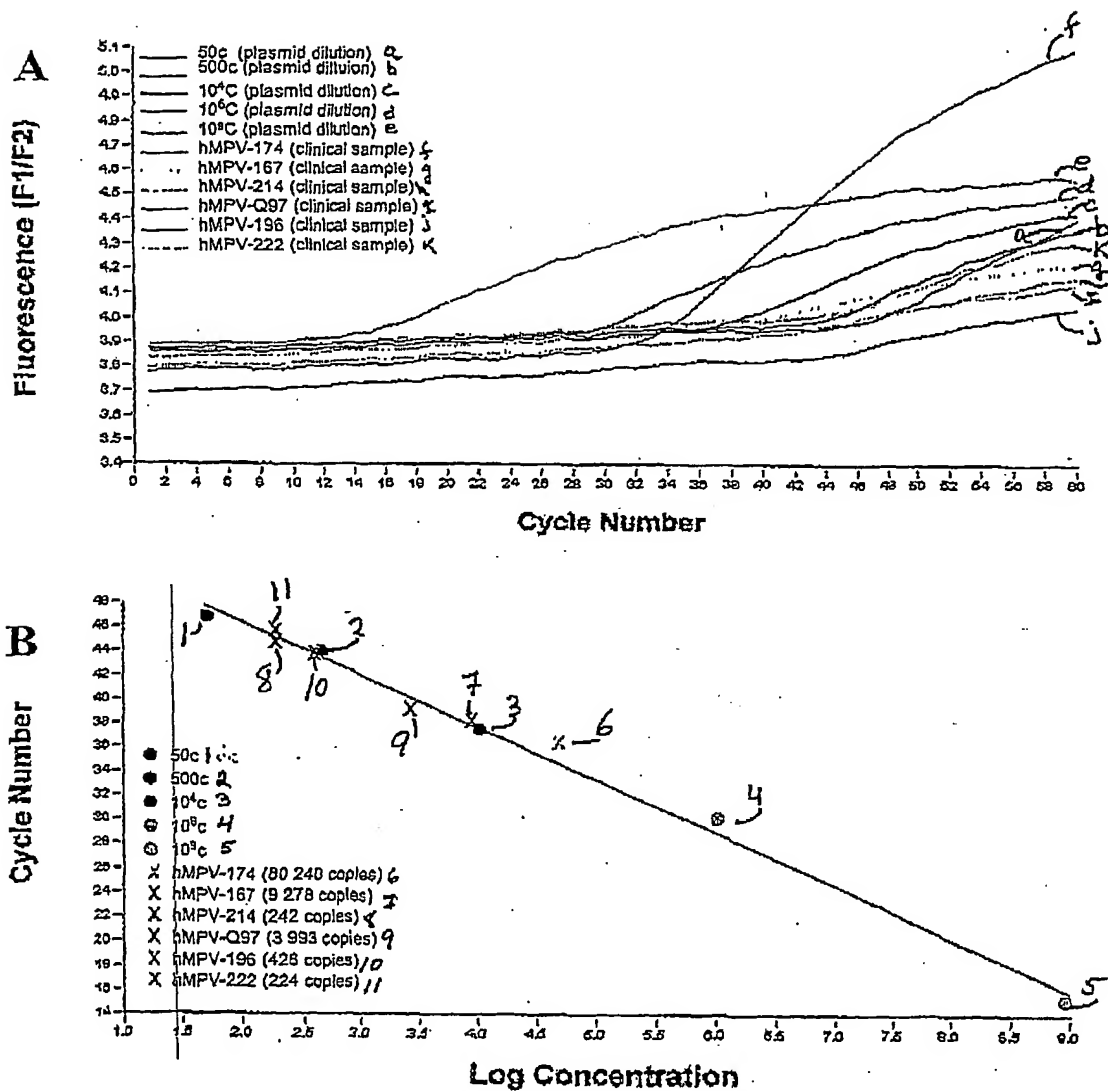


FIGURE 9

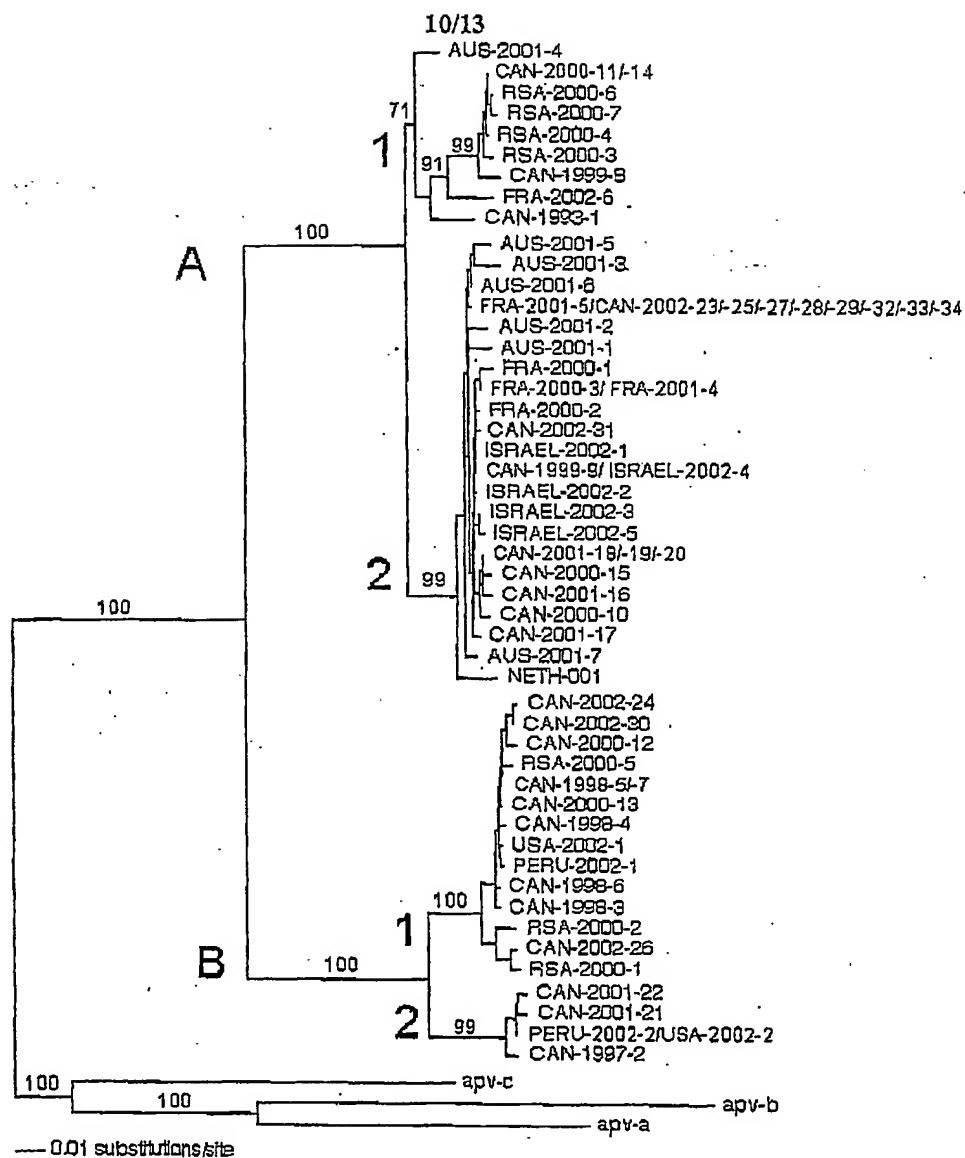


FIGURE 10 A

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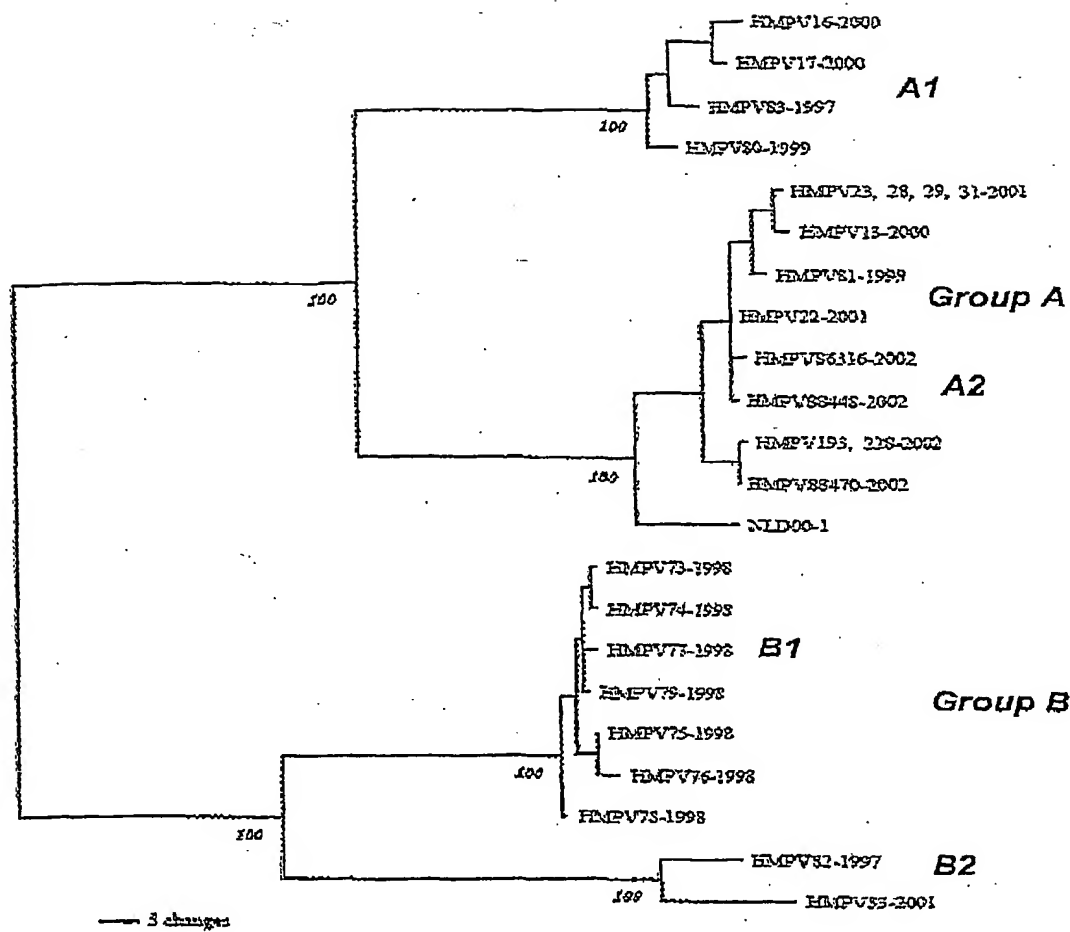


FIGURE 10 B

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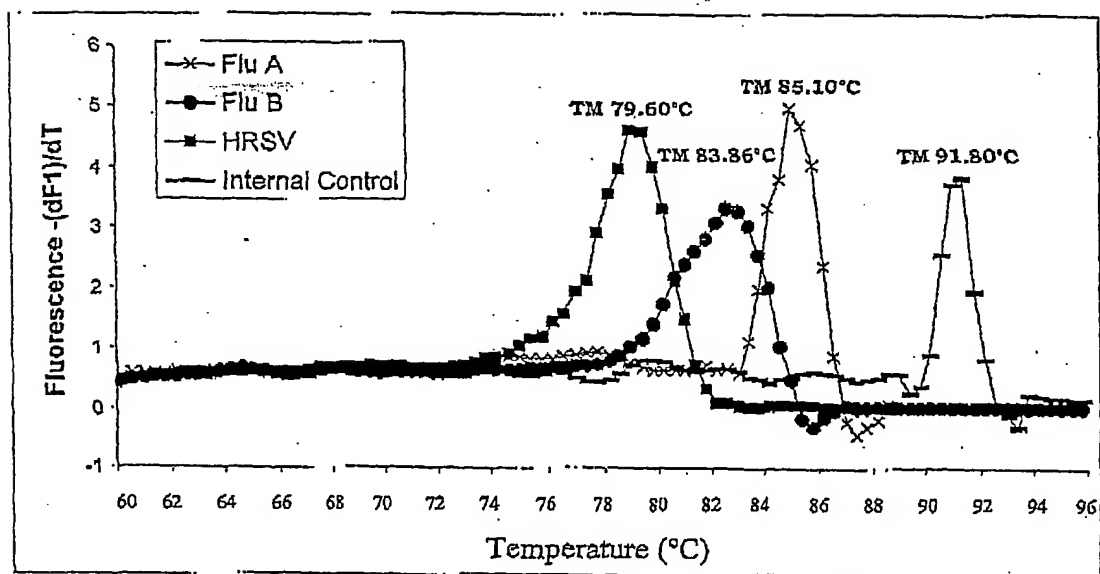


FIGURE 11

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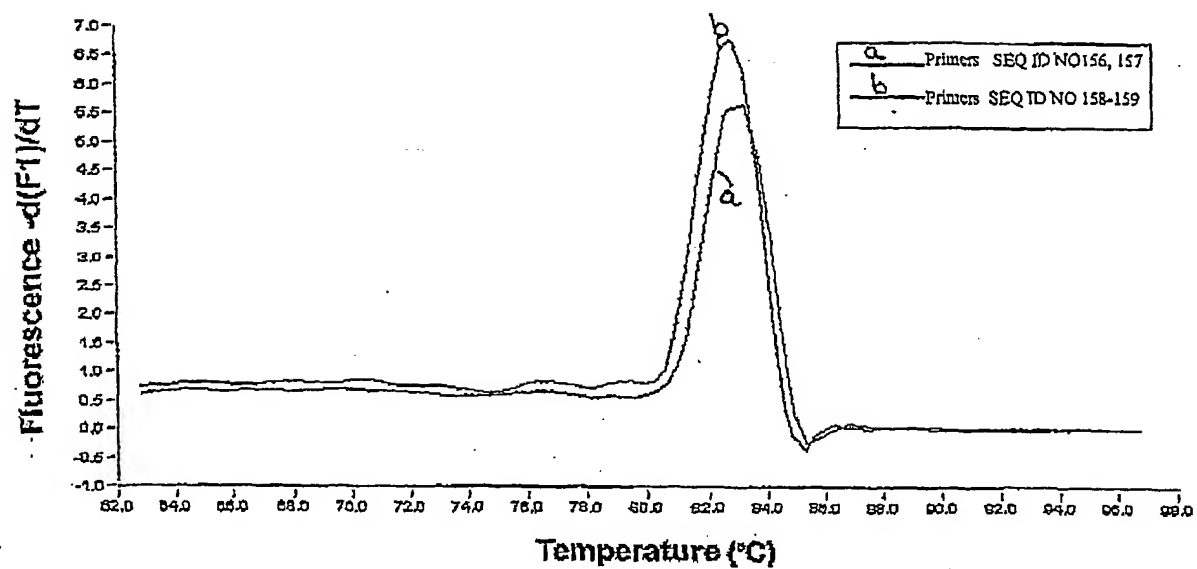


FIGURE 12

SEQUENCE LISTING

<110> Boivin, Guy

<120> METHOD FOR DETECTING RESPIRATORY VIRUSES

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<151> 2002-12-19

<150> CA 2,418,004

<151> 2003-01-24

<160> 172

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 13350

<212> DNA

<213> human metapneumovirus

<220>

<221> gene

<222> (1)...(13450)

<223> human metapneumovirus, strain 00-1
Accession number af371337

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<213> human metapneumovirus

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<222> (1)...(782)
<223> human metapneumovirus, strain Quebec isolate No
hMPV-118

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782

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<212> DNA
<213> human metapneumovirus

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<220>
<221> gene

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<210> 4
 <211> 876
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(876)
 <223> human metapneumovirus, strain Quebec Isolate No
 hmpv-176

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 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(869)
 <223> human metapneumovirus, strain Quebec Isolate No
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 <211> 850
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(850)
 <223> human metapneumovirus, strain Quebec Isolate No hMPV-217

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<210> 9
 <211> 1185
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<220>
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 <223> human metapneumovirus, strain 00-1, accession
 number af371337

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<220>
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 <223> human metapneumovirus, strain Quebec Isolate No
 hmpv-163

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 tttgttcatt gagtatggca aagcattagg ctcattcatc acagggcagca aagcagaaag 540
 tctatttgtt aatatattca tgcaagctta tggagccggt caaacaatgc taagggtggg 600

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ggtaattgcc aggtcatcca acaatataat gttaggacat gtatccgtcc aagctgagtt 660
 aaaacagggtc acagaagtct atgacttgggt gcgagaaatg 700

<210> 11
 <211> 705
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(705)
 <223> human metapneumovirus, strain Quebec Isolate No
 hMPV-174

<400> 11
 tattagcaca gctttaggat cagagagagt gcagcagatt ctgagggaact caggcagtga 60
 agtccaagtg gtcttaacca gaacgtactc tctggggaaa gttaaaaaca ataaaggaga 120
 agattttacag atgtttagaca tacacgggggt agagaagagc tgggtagaag agatagacaa 180
 agaagcaagg aaaacaattgg caaccttggct taagggaatca tcaggtaata tcccgcacaaa 240
 tcagaggccc tcagcaccag acacacccat aatcttatta tgtgtagggt ccttaatat 300
 tactaaacta gcatcaacca tagaagtggg actagagacc acagtcagaa gggctaaccg 360
 tgtactaagt gatgactca agagataccc tagaatggac atcccaaaaa ttgccagatc 420
 ctctcatgac ttatttgaac aaaaagtgtg tcacagaagt ttgttcattg agtatggcaa 480
 agcattaggc tcatcatcta caggcagcaa agcagaaagt gtattttgta atatattcat 540
 gcaagcttat ggagccggtc aaacaatgct gagggtggggg gtcatgtcca ggtcatccaa 600
 caatataatg ttaggacatg tatccgtcct agctgagcta aaaccggta cagaagtcta 660
 tgacttgggt cgagaaatga ttcttgaatc tngacttcta catta 705

<210> 12
 <211> 700
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(700)
 <223> human metapneumovirus, strain Quebec Isolate No
 hMPV-184

<400> 12
 aaatatgctg cagaaatagg aatacaatat attagcacag ctttaggac agagagagtg 60
 cagcagattc tgaggaaactc aggcagtgaa gtccaagtgg tcttaaccag aacgtactct 120
 ctgggggaaag ttaaaaacaa taaaggagaa gatttacaga tgttagacat acacggggta 180
 gagaagagct gggtagaaga gatagacaaa gaagcaagga aaacaatggc aaccttgctt 240
 aaggaatcat caggtaatat ccacacaaaat cagagggcct cagcaccaga cacaccata 300
 atcttattat gtgtagggtg ctttaatttt actaaactag catcaaccat agaagtggga 360
 ctagagacca cagtcagaag ggccaaccgt gtactaagt atgcaactca gagataccct 420
 agaattggata tcccaaaaat tgccagatcc ttctatgact tatttgaaca aaaagtgtat 480
 cacagaagtt tgttcattga gtatggcaca gcattaggct catcatctac aggcagcaaa 540
 gcagaaagtc tatttgttaa tataattcatg caagcttatg gagccggta aacaatgcta 600
 aggtgggggg taattgccag atcatccaac aatataatgt taggacatgt atccgtccaa 660
 gctgagttaa aacaggtcac agaagtctat gacttagtgc 700

<210> 13
 <211> 650
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(650)
 <223> human metapneumovirus, strain Quebec Isolate No
 hMPV-185

<400> 13
 taggaataga atatattagc acagctctag gatcagagag agtacagcag attctaagaa 60
 actcaggcag tgaagtccaa gtggttttaa ccagaacgta ctccrtgggg aaagrtaaaa 120
 acaacaaagg agaagattta cagatgttag acatacacgg agtagagaaa agctgggtgg 180
 aagagataga caaagaagca agaaaaacaa tggcaacttt gcttaagaa tcatcaggca 240
 atattccaca aaatcagagg ccttcagcac cagacacacc tataatctta ttatgtgtag 300
 gtgccttaat atttaccaaa ctagcatcaa ctatagaagt gggattagag accacagtca 360
 gaagagctaa ccgtgtacta agtgatgcac tcaaaagata ccctaggatg gacataccaa 420

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aaatcgcctag	atcttttctat	gacttatttg	aacaaaaagt	gtattacaga	agcttggttca	480
ttgagtatgg	caaagcatta	ggctcatcct	ctacaggcag	caaagcagaa	agttttattcg	540
ttaatatatt	catgcaagct	tacgggtgctg	gtcaacaat	gctgagggtg	ggagtcattg	600
ccagggtcatc	taacaatata	atgttaggac	atgtatctgt	ccaagctgag		650

<210> 14
 <211> 650
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(650)
 <223> human metapneumovirus, strain Quebec Isolate No C-76837

<400> 14	acaaatattgc	atcataaata	ggaatacaat	atattagcac	agcttttagag	atcagagaga	60
	gtgcagcaga	ttctaaggaa	ctcaggcag	gaagtcctaa	tggtcttaac	cagaacgtac	120
	tctctgggga	aagttaaaaa	caataaagga	gaagatttac	agatgttaga	catacacggg	180
	gtagagaaga	gctgggtaga	agagatagac	aaagaagcaa	ggaaaacaat	ggcaaccttg	240
	cttaagggaat	catcaggtaa	tatcccacaa	aatcagaggc	cctcagcacc	agacacaccc	300
	ataatcttat	tatgtgtagg	tgcccttaata	tttactaaac	tagcatcaac	catagaagtg	360
	ggactagaga	ccacagtcag	aagggtctaac	cgtgtactaa	gtgatgcact	caagagatac	420
	cctagaatgg	acatcccaaa	aattgccaga	tccttctatg	acttatrtga	acaaaaagtg	480
	tatcacagaa	gtttgttcat	tgagtatggc	aaagcattag	gctcatcatc	tacaggcagc	540
	aaagcagaaa	gtctatttgt	taatatatte	atgcaagctt	atggagccgg	tcaaaacaatg	600
	ctaagggtggg	gggtcattgc	cagggtcatcc	aacaatataa	tgtaggata		650

<210> 15
 <211> 650
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(650)
 <223> human metapneumovirus, strain Quebec Isolate No C-77807

<400> 15	gtatgctaaa	catgctgatt	acaaatattgc	tgacagaaata	ggaatacaat	atattagcac	60
	agcttttaga	tcagagagag	tgacagcagat	tctgaggaac	tcaggcagtg	aagtcctaat	120
	gggtcttaacc	agaacgtact	ctctggggaa	agttaaaaac	aataaaagga	gaagatttac	180
	agatgttaga	catacacggg	gtagagaaga	gctgggtaga	agagatagac	aaagaagcaa	240
	ggaaaaacaat	ggcaaccttg	cttaagggaat	catcaggtaa	tatcccacaa	aatcagaggc	300
	cctcagcacc	agacacaccc	ataatcttat	tatgtgtagg	tgcccttaata	tttactaagc	360
	tagcatcaac	catagaagtg	ggactagaga	ccacagtcag	aagggtctaac	cgtgtactaa	420
	gtgatgcact	caagagatac	cctagaatgg	acatcccaaa	aattgccaga	tccttctatg	480
	acttatrtga	acaaaaagtg	tatcacagaa	gtttgttcat	tgagtatggc	aaagcattag	540
	gctcatcatc	tacaggcagc	aaagcagaaa	gtctatttgt	taatatattc	atgcaagctt	600
	atggagccgg	tcaaaacaatg	ctaagggtggg	gggtcattgc	cagggtcatcc		650

<210> 16
 <211> 650
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(650)
 <223> human metapneumovirus, strain Quebec Isolate No hMPV-C-78123

<400> 16	ttaggatcag	agagagtgc	gcagattcta	aggaactcag	gcagtgaagt	ccaagtggc	60
	ttaaccagaa	cgtactctct	ggggaaaagt	aaaaacaata	aaggagaaga	tttacagatg	120
	ttagacatac	acggggtaga	gaagagctgg	gtagaagaga	tagacaaaaga	agcaaggaaa	180
	acaatggcaa	ccttgcctaa	ggaatcatca	ggtaatatcc	cacaaaaatca	gaggccctca	240
	gcaccagaca	caccataaat	cttattatgt	gtagggtgct	taatatrtac	taaacragca	300
	tcaaccatag	aagtgggact	agagaccaca	gtcagaaggg	ctaaccgtgt	actaagtgat	360
	gcactcaaga	gataccctag	aatggacatc	ccaaaaattg	ccagatcctt	ctatgactta	420

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tttgaacaaa aagtgtatca cagaagtttg ttcattgagt atggcaaac attaggctca 480
tcattctacag gcagcaaac agaaagtcta ttgttaata tattcatgca agcttatgga 540
gccgggtcaaa caatgctaag gtgggggggtc attgccaggt catccaacaa tataatgtta 600
ggacatgtat ccgtccaagc tgagttaaaa cagggtcacag aagttctatga 650

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<210> 17
 <211> 650
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(700)
 <223> human metapneumovirus, strain Quebec Isolate No C-78132

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<400> 17
cagaaagagt acaacagatt ttgagaaact caggtagtga agttcagggt gttttaacca 60
aaacatactc cttaggggaaa ggcaaaaaa gtaaaagggga agagctgcag atgttagata 120
tacatggagt ggaaaagagt tgggtagaag aaatagacaa agaggcaaga aagacaatgg 180
taactttgct taaggaggtca tcaggtaaca tccccaaaa ccagagacct tcagcaccag 240
acacaccaat aattttatta tgtgtagggt ccctaattat cactaaacta gcattctaca 300
tagaagttgg attagagact acagttagaa gagctaata agtgctaagt gatgcactca 360
aaagatacc tagggtagat ataccaaaaga ttgctagatc tttttatgaa ctatttgaac 420
aaaaagtgt ctacagaagt ttattcattg agtacggaaa agctttaggc tcattctcaa 480
caggaagcaa agcagaaagt ttgtttgtaa atatatatat gcaagcttat ggagctggtc 540
aaacactgct aaggtgggggt gtcattgccca gatcatccaa caacataatg ctagggcatg 600
tatctgtgca atctgaattg aagcaagtta cagaggttta tgacttggtg 650

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<210> 18
 <211> 650
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(650)
 <223> human metapneumovirus, strain Quebec Isolate No C-78163

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<400> 18
ggatcagaaa gagtacaaca gattttgaga aactcaggta gtgaagttca ggtggtttta 60
aacaaaacat actccttagg gaaaggcaaa aacagtaaa gggagagct gcagatgrra 120
gatatacatg gagtggaaaa gagttgggta gaagaaatag acaagaggc aagaaagaca 180
atggtaactt tgccttaagg gtcatcagggt aacatccac aaaaccagag accttcagca 240
ccagacacac caataatttt attatgtgta ggtgccctaa tattcactaa actagcatca 300
acaatagaag ttggattaga gactacagtt agaagagcta atagagtgtc aagtgatgca 360
ctcaaaaagt accctagggt agatatacca aagattgcta gatcttttta tgaactatct 420
gaacaaaaag tgtactacag aagttttattc attgagtacg gaaaagcttt aggcctcatc 480
tcaacaggaa gcaaaagcaga aagttttgttt gtaaatatat ttatgcaagc ttatggagct 540
ggccaacac tgctaagggt ggggtgtcatt gccagatcat ccaacaacat aatgctaggg 600
catgtatctg tgcaatctga attgaagcaa gttacagagg tttatgactt 650

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<210> 19
 <211> 600
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(600)
 <223> human metapneumovirus, strain Quebec Isolate No C-91205

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<400> 19
atattagcac agctctaggg atcagagaga gtacagcaga ttctaagaaa ctcaggcagt 60
gaagttccaa tggtttttaac cagaacgtac tccttggggga aagttaaaaa caacaaagga 120
gaagatttac agatgtttaga catacacgga gttagagaaaa gctgggtgga agagatagac 180
aaagaagcaa gaaaaacaat ggcaactttg cttaaagaat catcaggcaa tattccacaa 240
attcagaggg cttcagcacc agacacacct ataattttat tatgtgtagg tgccttaata 300
tttaccacac tagcatcaac tatagaagtg ggatttagaga ccacagtcag aagagctaac 360
cgtgtactaa gtgatgcact caaaagatgc cctaggatgg acataccaaa aatcgctaga 420

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 tctttctatg acttatttga acaaaaagtg tattacagaa gcttggtcat tgagtatggc 480
 aaagcattag gctcatctc tacaggcagc aaagcagaaa gtttattcgt taatatattc 540
 atgcaagctt acggtgctgg tcaaaacaatg ctgaggtggg gagtcattgc caggtcattc 600

<210> 20
 <211> 700
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(700)
 <223> human metapneumovirus, strain Quebec Isolate No C-91364

<400> 20
 gattacaaat atgctgctga gataggaatg caatatattt gcacagctct aggatcagaa 60
 agagtacaac agattttgag aaactcaggt agtgaagttc aggtggttct aaccaaaaca 120
 tactccttag ggaaaggcaa aaacagtaaa ggggaagagc tgcagatggt agatatacat 180
 ggagtggaag agagttgggt agaagaaata gacaaagagg caagaaagac aatggtaact 240
 ttgcttaagg agtcatcagg taacatccca caaaaccaga gaccttcagc accagacaca 300
 ccaataattt tattatgtgt aggtgcccta atattcacta aactagcatc aacaatagaa 360
 gttggattag agactacagt tagaagagct aatagagtgc taagtgatgc actcaaaaga 420
 taccctagggt tagatatacc aaagattgct agatcttttt atgaactatt tgaacaaaaa 480
 gtgtactaca gaagttttatt cattgagtag ggaaaagcct taggctcctc ttcaacagga 540
 agcaaaagcag aaagttttgt tgtaaatata tttatgcaag cttatggagc tgggtcaaca 600
 ctgctaaggt ggggtgtcat tgccagatca tccaacaaca taatgctagg gcatgtatct 660
 gtgcaatctg aattgaagca agttacagag gtttatgact 700

<210> 21
 <211> 600
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(600)
 <223> human metapneumovirus, strain quebec Isolate No C-91830

<400> 21
 cagctctagg atcagaaaaga gtacaacaga ttttgagaaa ctccaggtagt gaagttcagg 60
 tggtttctaac caaaacatac tccttaggga aaggcaaaaa cagtaaagggt gaagagctgc 120
 agatgttaga tatacatgga gtggaaaaga gttgggtaga agaaatagac aaagaggcaa 180
 gaaagacaat ggtaactttg ctttaaggagt catcaggtaa catcccaaca aaccagagac 240
 cticagcacc agacacacca ataattttat tatgtgtagg tgccttaata ttcactaaac 300
 tagcatcaac aatagaagtt ggattagaga ctacagttag aagagctaata agagtgtctaa 360
 gtgatgcact caaaagatac cctagggttag atataccaaa gattgctaga tctttttatg 420
 aactatttga acaaaaagtg tactacagaa gcttattcat tgagtacgga aaagcttttag 480
 gctcatcttc aacaggaagc aaagcagaga gtttgtrtgt aaatatattt atgcaagcct 540
 atggagctgg tcaaacactg ctaagggtggg gtgtcattgc cagatcatcc aacaacataa 600

<210> 22
 <211> 650
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(650)
 <223> human metapneumovirus, strain Quebec Isolate No hMPV-Q86

<400> 22
 atgctgatta caaatatgct gcagaaatag gaatacaata tattagcaca gctctagggt 60
 cagagaaaagt acagcagatt ctaagaaact caggcagtga agtccaagcg gttttaacca 120
 gaacgtactc rrrggggaaa gtttaaaaaa ataaaggaga agatttcacag atgttagaca 180
 tacacggagt agaaaaaagc tgggtggaag agatagacaa agaaagcaaga aaaacaatgg 240
 caactttact taaagaatca tcaggtaata tcccaaaaaa tcagaggcct tcagcaccag 300
 acacacctat aatcttatta tgtgtagggt ccttaatat caccaaaacta gcatcaacta 360
 tagaagtggg attagagacc acagtcagaa gagctaaccg tgtactaagt gatgcactca 420
 aaagataccc tagaatggac ataccaaaaa ttgctagatc cttctargac ttatttgaac 480

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aaaaagtgtgta	tcacagaagt	ttgttcattg	agtatgggca	aagcattagg	ctcatcctct	540
acaggcagca	aagcagaaaag	tttattcgtc	aatatattca	tgcaagctta	tggtgctggg	600
caacaatgc	tgagggtggg	gggttatcgc	caggtcatct	aacaatataa		650

<210> 23
 <211> 650
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(650)
 <223> human metapneumovirus, strain Quebec Iso|ate No
 hMPV-Q97

<400> 23						
tagcacagct	ctaggatcag	agagagtaca	gcagattcta	agaaactcag	gcagtgaagt	60
ccaagtgggt	ttaaccagaa	cgtactcctt	ggggaaaagt	aaaaacaaca	aaggagaaga	120
tttacagatg	ttagacatac	acggagtaga	gaaaagctgg	gtgggaagaga	tagacaaaga	180
agcaagaaaa	acaatggcaa	cttggcttaa	agaatcatca	ggcaatattc	cacaaaatca	240
gaggccttca	gcaccagaca	cacctataat	cttattatgt	gtagggtgcct	taatatattac	300
caaaactagca	tcaactatag	aagtgggatt	agagaccaca	gtcagaagag	ctaaccgtgt	360
actaagtgat	gcactcaaaa	gataccctag	gatggacata	ccaaaaatcg	ctagatctttt	420
ctatgactta	tttgacaaca	aagtgtatta	cagaagcttg	ttcattgagt	atggcaaagc	480
atttaggtca	tcctctacag	gcagcaaaagc	agaaaagttt	attcggttaat	atattcatgc	540
aagcttacgg	tgctgggtcaa	acaatgctga	ggtggggagt	cattgccagg	tcattctaaca	600
atataatggt	aggacatgta	tctgtccaag	ctgagttaaa	acaagtcacg		650

<210> 24
 <211> 741
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(741)
 <223> human metapneumovirus, strain Can 97-83

<400> 24						
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taagcatgct	gattacaaat	atgctgcaga	aataaggaata	caatatatta	gcacagctct	120
aggatcagag	agagtacagc	agattctaag	aaactcaggg	agtgaagtc	aagtgggtttt	180
aaccagaaag	tactccttgg	ggaaaagttaa	aaacaacaaa	ggagaagatt	tacagatggt	240
agacatacac	ggagttagaga	aaagctgggt	ggaagagata	gacaaagaag	caagaaaaac	300
aatggcaact	ttgcttaaa	aatcatcagg	caatatctca	caaaatcaga	ggccttcagc	360
accagacaca	cctataatct	tattatgtgt	aggtgcttta	atattttacca	aactagcatc	420
aactatagaa	tggtggattag	agaccacagt	cagaagagct	aaccgtgtac	taagtgatgc	480
actcaaaaaga	tacccttagga	tggaacatacc	aaaaatcgct	agatctttct	atgatttatt	540
tgaaacaaaa	gtgtattaca	gaagtttggt	cattgagtat	ggcaaaagcat	taggtctatc	600
ctctacaggc	agcaaaagcag	aaagtttatt	cgttaatata	ttcatgcaag	cttacgggtgc	660
tggtcaaaaca	atgctgaggt	ggggagtcac	tgccagggtca	tctaacaata	taatgttagg	720
acatgtatct	gtccaagctg	a				741

<210> 25
 <211> 650
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(650)
 <223> human metapneumovirus, strain Can 98-75

<400> 25						
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agtgaagttc	agggtgggtct	aaccaagaca	tacicttttag	ggaaaggtta	aaatagtaaa	120
ggggaagagt	tgcaaatggt	agatatcat	ggagtggaaa	agagttgggt	agaagaaata	180
gacaaagagg	caagaaaaaac	aatgggtgact	ttgttaaagg	aatcatcagg	taacatccca	240
caaaaccaga	ggccttcagc	accagacaca	ccaataattt	tattatgtgt	agggtcttta	300
atattcacta	aactagcatc	aacaatagaa	gttggactag	agactacagt	tagaagagct	360
aacagagtgc	taagtgatgc	gctcaaaaaga	taccctaggg	tagatatacc	gaagattgct	420
agatctttct	atgaactatt	tgagcagaaa	gtgtattaca	ggagtctatt	cattgagtat	480

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gggaaagcct taggctcatc ttcaacagga agcaaagcag aaagtttgtt tgtaaatata 540
tttatgcaag cttatggagc cggtaaaaca atgctaagggt ggggtgtcat tgccagatca 600
tctaacaaca taatgctagg acatgtgtct gtgcaagctg aattgaagca 650

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<210> 26
 <211> 759
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(759)
 <223> human metapneumovirus, strain Can 98-75

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<400> 26
atgtcttggg aagtgggtgat tatcatttcg ttactcataa cacctcagca cggactaaaa 60
gaaagttatt tagaagaatc atgtagtact ataactgaag gatattctag tgttttaaga 120
acagggttgg acaccaatgt ctttacatta gaagttgggt atgttgaaaa tcttacatgt 180
actgatggac ctatgcttaac caaaacagaa cttgacctaa ccaaaagtgc tctaagagaa 240
ctcaaaacag tttctgtcga tcagtttagc agagaagaac aaattgaaa tcccagacaa 300
tcaagggttt tcctagggtgc aatagctctt ggtgttgcca cagcagcagc agtcacagca 360
ggcatttgca tagccaaaac cataaggctt gagagtgaag tgaatgcaat caaagggtgt 420
ctcaaaacaa ccaacgagggc agtatccaca ctaggaaatg gagtgcgagt cctagccacc 480
gcagtaagag agctgaaaga atttgtgagc aaaaacctga ctagtgcatt taacaagaac 540
aaatgtgaca ttgtgcacct gaagatggct gtcagcttca gtcaattcaa cagaagattc 600
ctaaatgttg tgcggcagtt ttcagacaat gcagggataa caccagcaat atcattggac 660
ctaattgact atgctgagct ggccagagct gtatcatata tgccaacatc tgcaggacag 720
ataaaactaa tgttagagaa ccgtgcaatg gtaagaaga 759

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<210> 27
 <211> 759
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(759)
 <223> human metapneumovirus, strain Quebec Isolate No C-67345

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<400> 27
atgtcttggg aagtgggtgat cattttttca ttgcraataa caccctcaaca cggctcttaaa 60
gagagctacc tagaagaatc atgtatcact ataactgagg gatattcttag tgttctgaga 120
acagggttgg ataccaacgt ttttacatta gaggtgggtg atgtagaaaa ccttacatgt 180
tctgatggac ctagcctaac aaaaacagaa ttagatctga ccaaaagtgc actaagagag 240
ctcaaaacag tctctgtcga ccaatttgga agagaggaaac aaattgagaa tcccagacaa 300
tctaggtttg ttctgggagc aatagcactc ggtgttgcaa cagcagctgc agtcacagca 360
ggtgttgcaa ttgcccacaa catccggctt gagagtgaag tcacagcaat taagaatgcc 420
ctcaaaacga ccaatgaagc agtatctaca ttggggaaatg gagttcgagt gttggcaact 480
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ctaaatgttg tgcggcaatt ttcagacaat gctggaataa caccagcaat atctttggac 660
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<210> 28
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<220>
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 <222> (1)...(759)
 <223> human metapneumovirus, strain Can 97-83

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ttggacttaa	tgacagatgc	tgaactagcc	agggccggtt	ctaactgcc	gacatctgca	720
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 <222> (1)...(759)
 <223> human metapneumovirus, strain quebec Isolate No
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<220>
 <221> gene
 <222> (1)...(759)
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<220>
 <221> gene
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<400> 31

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ttaatgacag	atgctgaact	agccagggcc	gtttctaaca	tgccgacatc	tcaggagcaa	720
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acaggttggg	ataccaacgt	ttttacatta	gaggtgggtg	atgtagaaaa	ccttacatgt	180
tctgatggac	ctagcctaata	aaaaacagaa	ttagatctga	ccaaaagtgc	actaagagag	240
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ggtgttgcaa	ttgccaaaac	catccggctt	gagagtgaag	tcacagcaat	taagaatgcc	420
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ctcagaacag	tttctgctga	tcaactggca	agagaggagc	aaattgagaa	tcccagacaa	300
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ctcaaaaaga	ccaatgaagc	agratctaca	ttgggggaatg	gagttcgagt	gttggcaact	480
gcagtggagg	aactgaaaaga	ttttgtgagc	aagaatctaa	cacgtgcaat	caacaaaaac	540
aagtgcgaca	ttgctgacct	gaaaatggcc	gttagcttca	gtcaattcaa	cagaaggrrt	600
ctaaatgttg	tgcggaatt	ttcagacaat	gctggaataa	caccacacat	atccttggac	660
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<210> 34
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<220>

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<221> gene
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 <223> human metapneumovirus, strain Quebec Isolate No
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	gcagtgaagg	agctgaaaga	ttttgtgagc	aagaatctaa	cacgtgcaat	caacaaaaac	540
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	ttaatgacag	atgctgaact	agccagagct	gtttccaaca	tgccaacatc	tgaggacaa	720
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<220>
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 <222> (1)...(759)
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	gctgatggac	ctagcttaat	aaaaacagaa	ttagactctga	ccaaaagtgc	actaagagag	240
	ctcagaacag	tttctgctga	tcaactggca	agagaggagc	aaattgagaa	tcccagacaa	300
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	ggtgttgcaa	ttgccaaaac	catccggcct	gaaagtgaag	taacagcaat	taagaatgcc	420
	ctcaaaaaga	ccaatgaagc	agratctaca	ttgggggaatg	gagttcgagt	gttggcaact	480
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	ctaaatgttg	tgcggaactt	ttcagacaat	gctggaataa	caccagcaat	atccttggac	660
	ttaatgacag	atgctgaact	agccagagct	gtttccaaca	tgccaacatc	tgaggacaa	720
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	gctgatggac	ctagcttaat	aaaaacagaa	ttagactctga	ccaaaagtgc	actaagagag	240
	ctcagaacag	tttctgctga	tcaactggca	agagaggagc	aaattgagaa	tcccagacaa	300
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	ttaatgacag	atgctgaact	agccagagct	gtttccaaca	tgccaacatc	tgaggacaa	720
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 acaggttggg ataccaacgt ttttacctg gaggtagggt atgtagagaa ctttacatgt 180
 gctgatggac ctactttaat aaaaacagaa ttagatctga ccaaaagtgc actaagagag 240
 ctcaagaacag tttctgtctga tcaactggca agagaggagc aaattgagaa tcccagacaa 300
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 ggtgttgcaa ttgccaaaac catccggctt gaaagtgaag taacagcaat taagaatgcc 420
 ctcaaaaaga ccaatgaagc agtatctaca ttgggggaatg gagttcgagt gttggcaact 480
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<210> 38
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 <213> human metapneumovirus

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 <221> gene
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 ctcaagaacag tttctgtctga tcaactggca agagaggagc aaattgagaa tcccagacaa 300
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 acaggttggg ataccaacgt ttttacctg gaggtagggt atgtagagaa ctttacatgt 180
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 ggtgttgcaa ttgccaaaac catccggctt gaaagtgaag taacagcaat taagaatgcc 420
 ctcaaaaaga ccaatgaagc agtatctaca ttgggggaatg gagttcgagt gttggcaact 480

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gcagtgagag	agctgaaaga	ttttgtgagc	aagaatctaa	cacgtgcaat	caacaaaaac	540
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ttaatgacag	atgctgaact	agccagagct	gtttccaaca	tgccaacatc	tgaggacaa	720
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<220>
 <221> gene
 <222> (1)...(759)
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 <221> gene
 <222> (1)...(759)
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aagtgcgaca	ttgtcgacct	gaaaatggcc	gttagcttca	gtcaattcaa	cagaagggtt	600
ctaaatgttg	tgcggaacat	ttcagacaat	gctggaataa	caccagcaat	atccttggac	660
ttaatgacag	atgctgaact	agccagagct	gtttccaaca	tgccaacatc	tgaggacaa	720
ataaaactga	tggtggagaa	ccgtgcaatg	gtaagaaga			759

<210> 42
 <211> 759
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(759)
 <223> human metapneumovirus, strain Quebec Isolate No
 hMPV-198

<400> 42						
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gagagctatt	tagaagagtc	atgtagcact	ataactgaag	gatattctag	tggtctgagg	120

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acagggttgg	ataccaacgt	ttttacactg	gaggtaggtg	atgtagagaa	ccttacatgt	180
gctgatggac	ctagcttaat	aaaaacagaa	ttagacctga	ccaaaagtgc	actaagagag	240
ctcagaacag	ttttctgctga	tcaactggca	agagaggagc	aaattgagaa	tcccagacaa	300
tctagatttg	ttctaggagc	aatagcactc	ggtgttgcaa	cagcagctgc	agttacagca	360
ggtgttgcaa	ttgccaaaac	catccggctt	gaaagtgaag	taacagcaat	taagaatgcc	420
ctcaaaaaga	ccaatgaagc	agtatctaca	ttgggggaatg	gagttcgagt	gttggcaact	480
gcagtggagag	agctgaaaaga	ttttgtgagc	aagaatctaa	cacgtgcaat	caacaaaaac	540
aagtgcgaca	ttgtgacct	gaaaatggcc	gttagcttca	gtcaattcaa	cagaagggtt	600
ctaaatgttg	tgcggcaatt	ttcagacaat	gctggaataa	caccagcaat	atccttggac	660
ttaatgacag	atgctgaact	agccagagct	gtttccaaca	tgccaacatc	tgaggacaa	720
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<210> 43
 <211> 759
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(759)
 <223> human metapneumovirus, strain Quebec Isolate No
 hMPV-217

<400> 43						
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acagggttgg	ataccaacgt	ttttacactg	gaggtaggtg	atgtagagaa	ccttacatgt	180
gctgatggac	ctagcttaat	aaaaacagaa	ttagacctga	ccaaaagtgc	actaagagag	240
ctcagaacag	ttttctgctga	tcaactggca	agagaggagc	aaattgagaa	tcccagacaa	300
tctagatttg	ttctaggagc	aatagcactc	ggtgttgcaa	cagcagctgc	agttacagca	360
ggtgttgcaa	ttgccaaaac	catccggctt	gaaagtgaag	taacagcaat	taagaatgcc	420
ctcaaaaaga	ccaatgaagc	agtatctaca	ttgggggaatg	gagttcgagt	gttggcaact	480
gcagtggagag	agctgaaaaga	ttttgtgagc	aagaatctaa	cacgtgcaat	caacaaaaac	540
aagtgcgaca	ttgtgacct	gaaaatggcc	gttagcttca	gtcaattcaa	cagaagggtt	600
ctaaatgttg	tgcggcaatt	ttcagacaat	gctggaataa	caccagcaat	atccttggac	660
ttaatgacag	atgctgaact	agccagagct	gtttccaaca	tgccaacatc	tgaggacaa	720
ataaaaactga	tggtggagaa	ccgtgcaatg	gtaagaaga			759

<210> 44
 <211> 759
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(759)
 <223> human metapneumovirus, strain Quebec Isolate No
 hMPV-208

<400> 44						
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acagggttgg	ataccaacgt	ttttacactg	gaggtaggtg	atgtagagaa	ccttacatgt	180
gctgatggac	ctagcttaat	aaaaacagaa	ttagacctga	ccaaaagtgc	actaagagag	240
ctcagaacag	ttttctgctga	tcaactggca	agagaggagc	aaattgagaa	tcccagacaa	300
tctagatttg	ttctaggagc	aatagcactc	ggtgttgcaa	cagcagctgc	agttacagca	360
ggtgttgcaa	ttgccaaaac	catccggctt	gaaagtgaag	taacagcaat	taagaatgcc	420
ctcaaaaaga	ccaatgaagc	agtatctaca	ttgggggaatg	gagttcgagt	gttggcaact	480
gcagtggagg	agctgaaaaga	ttttgtgagc	aagaatctaa	cacgtgcaat	caacaaaaac	540
aagtgcgaca	ttgtgacct	gaaaatggcc	gttagcttca	gtcaattcaa	cagaagggtt	600
ctaaatgttg	tgcggcaatt	ttcagacaat	gctggaataa	caccagcaat	atccttggac	660
ttaatgacag	atgctgaact	agccagagct	gtttccaaca	tgccaacatc	tgaggacaa	720
ataaaaactga	tggtggagaa	ccgtgcaatg	gtaagaaga			759

<210> 45
 <211> 759
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(759)

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<223> human metapneumovirus, strain Quebec Isolate No
hmpv-223

<400> 45

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acaggtttgg	ataccaacgt	ttttacactg	gaggtagggtg	atgttagagaa	ccttacatgt	180
gctgatggac	ctagcttaaat	aaaaacagaa	ttagacctga	ccaaaagtgc	actaagagag	240
ctcagaacag	tttctgctga	tcaactggca	agagaggagc	aaattgagaa	tcccagacaa	300
tctagatttg	ttctaggagc	aatagcactc	ggtgttgcaa	cagcagctgc	agttacagca	360
ggtgttgcaa	ttgccaaaac	catccggctt	gaaagtgaag	taacagcaat	taagaatgcc	420
ctcaaaaaga	ccaatgaagc	agtatctaca	ttggggaaatg	gagttcgagt	gttggcaact	480
gcagtggagag	agctgaaaga	ttttgtgagc	aagaatctaa	cacgtgcaat	caacaaaaac	540
aagtgcgaca	ttgtgcacct	gaaaatggcc	gttagcttca	gtcaattcaa	cagaagggtt	600
ctaaatggtt	tgcggaatt	ttcagacaat	gctggaataa	caccagcaat	atccttggac	660
ttaatgacag	atgtggaact	agccagagct	gtttccaaca	tgccaacatc	tgaggacaa	720
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<210> 46

<211> 759

<212> DNA

<213> human metapneumovirus

<220>

<221> gene

<222> (1)...(759)

<223> human metapneumovirus, strain Quebec Isolate No
hmpv-228

<400> 46

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acaggtttgg	ataccaacgt	ttttacactg	gaggtagggtg	atgttagagaa	ccttacatgt	180
gctgatggac	ctagcttaaat	aaaaacagaa	ttagacctga	ccaaaagtgc	actaagagag	240
ctcagaacag	tttctgctga	tcaactggca	agagaggagc	aaattgagaa	tcccagacaa	300
tctagatttg	ttctaggagc	aatagcactc	ggtgttgcaa	cagcagctgc	agttacagca	360
ggtgttgcaa	ttgccaaaac	catccggctt	gaaagtgaag	taacagcaat	taagaatgcc	420
ctcaaaaaga	ccaatgaagc	agtatctaca	ttggggaaatg	gagttcgagt	gttggcaact	480
gcagtggagag	agctgaaaga	ttttgtgagc	aagaatctaa	cacgtgcaat	caacaaaaac	540
aagtgcgaca	ttgtgcacct	gaaaatggcc	gttagcttca	gtcaattcaa	cagaagggtt	600
ctaaatggtt	tgcggaatt	ttcagacaat	gctggaataa	caccagcaat	atccttggac	660
ttaatgacag	atgtggaact	agccagagct	gtttccaaca	tgccaacatc	tgaggacaa	720
ataaaactga	tggtggagaa	ccgtgcaatg	gtaagaaga			759

<210> 47

<211> 759

<212> DNA

<213> human metapneumovirus

<220>

<221> gene

<222> (1)...(759)

<223> human metapneumovirus, strain Quebec Isolate No
C-85885

<400> 47

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gagagctatt	tagaagagtc	atgttagcact	ataactgaag	gatatctcag	tggtctgagg	120
acaggtttgg	ataccaacgt	ttttacactg	gaggtagggtg	atgttagagaa	ccttacatgt	180
gctgatggac	ctagcttaaat	aaaaacagaa	ttagacctga	ccaaaagtgc	actaagagag	240
ctcagaacag	tttctgctga	tcaactggca	agagaggagc	aaattgagaa	tcccagacaa	300
tctagatttg	ttctaggagc	aatagcactc	ggtgttgcaa	cagcagctgc	agttacagca	360
ggtgttgcaa	ttgccaaaac	catccggctt	gaaagtgaag	taacagcaat	taagaatgcc	420
ctcaaaaaga	ccaatgaagc	agtatctaca	ttggggaaatg	gagttcgagt	gttggcaact	480
gcagtggagag	agctgaaaga	ttttgtgagc	aagaatctaa	cacgtgcaat	caacaaaaac	540
aagtgcgaca	ttgtgcacct	gaaaatggcc	gttagcttca	gtcaattcaa	cagaagggtt	600
ctaaatggtt	tgcggaatt	ttcagacaat	gctggaataa	caccagcaat	atccttggac	660
ttaatgacag	atgtggaact	agccagagct	gtttccaaca	tgccaacatc	tgaggacaa	720
ataaaactga	tggtggagaa	ccgtgcaatg	gtaagaaga			759

<210> 48

<211> 759

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<212> DNA
 <213> human metapneumovirus

<220> gene
 <221> (1)...(759)
 <223> human metapneumovirus, strain Quebec Isolate No
 C-60298

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<400> 48
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gagagctattc tagaagagatc atgttagcact ataactgaag gatattctcag tgttctgagg 120
acagggttggg ataccaacgt ttttaacttg gaggtagggtg atgtagagaa ccttacatgt 180
gctgatgggac ctatgcttaat aaaaacagaa ttagatctga ccaaaagtgc actaagagag 240
ctcagaacag tttctgctga tcaactggca agagaggagc aaattgagaa tcccagacaa 300
tctagatttg ttctaggagc aatagcactc ggtgttgcaa cagcagctgc agttacagca 360
gggtgttgcaa ttgccaaaac catccggctt gaaagtgaag taacagcaat taagaatgcc 420
ctcaaaaaga ccaatgaagc agtatctaca ttggggaaatg gagttcgagt gttggcaact 480
gcagtggaggg aactgaaaga tttgtgagc aagaatctaa cacgtgcaat caacaaaaac 540
aagtgcgaca ttgctgacct gaaaatggcc gtttagcttca gtcaattcaa cagaagggtt 600
ctaaatgttg ttgcggcaatt ttcagacaat gctggataaa caccagcaat atcttggac 660
ttaatgacag atgctgaact agccagagct gtttccaaca tgccaacatc tgcaggacaa 720
ataaaactga tgttgagaa cctgtgcaatg gtaagaaga 759
  
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<210> 49
 <211> 759
 <212> DNA
 <213> human metapneumovirus

<220> gene
 <221> (1)...(759)
 <223> human metapneumovirus, strain Quebec Isolate No
 C-63778

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<400> 49
atgtcttggga aagtgggtgat tatcatttcg ttactcataa caccctcagca cggactaaaag 60
gaaagttatt tagaagaatc atgtagtact ataactgaag gatattctcag tgttttaaga 120
acagggttggg acaccaatgt ctttacatta gaagttgggtg atgttgaaaa tcttacatgt 180
actgatgggac ctatgcttaat caaaacagaa cttgacctaa ccaaaagtgc tctaagagaa 240
ctcaaaaacag tttctgctga tcagttagcg agagaagaac aaattgaaaa tcccagacaa 300
tcaagggtttg tcctagggtgc aatagctctt ggtgttgcca cagcagcagc agtcacagca 360
ggcattgcca tagccaaaac cataaggcctt gagagtgaag tgaatgcaat caaagggtgt 420
ctcaaaaacaa ccaacgagggc agtatccaca ctaggaaatg gagtgcgagt cctagccacc 480
gcagttaagag agctgaaaga atttgtgagc aaaaacctga ctagtcaat taacaagaac 540
aaatgtgaca ttgctgatct gaagatggct gtcagcttca gtcaattcaa cagaagattc 600
ctaaatgttg ttgcggcagtt ttcagacaat gcagggataa caccagcaat atcattggac 660
ctaatgactg atgctgagct ggccagaact gtatcatata tgccaacatt tgcaggacag 720
ataaaactaa tgttagagaa cctgtgcaatg gtaagaaga 759
  
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<210> 50
 <211> 759
 <212> DNA
 <213> human metapneumovirus

<220> gene
 <221> (1)...(759)
 <223> human metapneumovirus, strain Quebec Isolate No
 C-64199

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gaaagttatt tagaagaatc atgtagtact ataactgaag gatattctcag tgttttaaga 120
acagggttggg acaccaatgt ctttacatta gaagttgggtg atgttgaaaa tcttacatgt 180
actgatgggac ctatgcttaat caaaacagaa cttgacctaa ccaaaagtgc tctaagagaa 240
ctcaaaaacag tttctgctga tcagttagcg agagaagaac aaattgaaaa tcccagacaa 300
tcaagggtttg tcctagggtgc aatagctctt ggtgttgcca cagcagcagc agtcacagca 360
ggcattgcca tagccaaaac cataaggcctt gagagtgaag tgaatgcaat caaaggatgt 420
ctcaaaaacaa ccaacgagggc agtatccaca ctaggaaatg gagtgcgagt cctagccacc 480
gcagttaagag agctgaaaga atttgtgagc aaaaacctga ctagtcaat taacaagaac 540
aaatgtgaca ttgctgatct gaagatggct gtcagcttca gtcaattcaa cagaagattc 600
  
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ctaaatgttg tgcggcagtt ttcagacaat gcagggataa caccagcaat atcattggac	660
ctaattgactg atgctgagct ggcagagct gtatcataca tgccaacatc tgcaggacag	720
ataaaactaa tgttagagaa ccgtgcaatg gtaagaaga	759

<210> 51
 <211> 759
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(759)
 <223> human metapneumovirus, strain Quebec Isolate No C-64200

<400> 51 atgtcttgga aagtggatgat tatcatttcg ttactcataa caccctcagca cggactaaaa	60
gaaagtatt tagaagaatc atgtagtact ataactgaag gatattctcag tgttttaaga	120
acaggttggt acaccaatgt ctttacatta gaagttgggt atgttgaaaa tcttacatgt	180
actgatggac ctatgcttaat caaaacagaa cttgacctaa ccaaaagtgc tctaagagaa	240
ctcaaaacag tttctgctga tcagtttagcg agagaagaac aaattgaaaa tcccagacaa	300
tcaaggtttg tcctaggtgc aatagctctt ggtgttgcca cagcagcagc agtcacagca	360
ggcattgcga tagcctaaac cataaggctt gagagtgaag tgaatgcaat caaagggtgc	420
ctcaaaacaa ccaacgaggg agtatccaca ctaggaaatg gagtgcgagt cctagccacc	480
gcagtaagag agctgaaaga atttgtgagc aaaaacctga ctagtgcatt taacaagaac	540
aaatgtgaca ttgctgatct gaagatggct gtcagcttca gtcaattcaa cagaagattc	600
ctaaatgttg tgcggcagtt ttcagacaat gcagggataa caccagcaat atcattggac	660
ctaattgactg atgctgagct ggcagagct gtatcataca tgccaacatc tgcaggacag	720
ataaaactaa tgttagagaa ccgtgcaatg gtaagaaga	759

<210> 52
 <211> 759
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(759)
 <223> human metapneumovirus, strain Quebec Isolate No C-64536

<400> 52 atgtcttgga aagtggatgat tatcatttcg ttactcataa caccctcagca cggactaaaa	60
gaaagtatt tagaagaatc atgtagtact ataactgaag gatattctcag tgttttaaga	120
acaggttggt acaccaatgt ctttacatta gaagttgggt atgttgaaaa tcttacatgt	180
actgatggac ctatgcttaat caaaacagaa cttgacctaa ccaaaagtgc tctaagagaa	240
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tcaaggtttg tcctaggtgc aatagctctt ggtgttgcca cagcagcagc agtcacagca	360
ggcattgcga tagcctaaac cataaggctt gagagtgaag tgaatgcaat caaagggtgc	420
ctcaaaacaa ccaacgaggg agtatccaca ctaggaaatg gagtgcgagt cctagccacc	480
gcagtaagag agctgaaaga atttgtgagc aaaaacctga ctagtgcatt taacaagaac	540
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ctaaatgttg tgcggcagtt ttcagacaat gcagggataa caccagcaat atcattggac	660
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ataaaactaa tgttagagaa ccgtgcaatg gtaagaaga	759

<210> 53
 <211> 759
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(759)
 <223> human metapneumovirus, strain Quebec Isolate No C-73769

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ccaggttggt acaccaatgt ctttacatta gaagttgggt atgttgaaaa tcttacatgt	180
actgatggac ctatgcttaat caaaacagaa cttgacctaa ccaaaagtgc tctaagagaa	240

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ctcaaaacag	tttctgctga	tcagttagcg	agagaagaac	aaattgaaaa	tcccagacaa	300
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ggcattgcga	tagccaaaac	cataaggctt	gagagtgaag	tgaatgcaat	caaagggtgct	420
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gcagtaagag	agttgaaaga	atttgtgagc	aaaaacctga	ctagtgcatt	taacaagaac	540
aaatgtgaca	ttgctgatct	gaagatggct	gtcagcttca	gtcaattcaa	cagaagattc	600
ctaaatgttg	tgcggcagtt	ttcagacaat	gcagggataa	caccagcaat	atcatttagac	660
ctaattgactg	atgctgagct	ggccagagct	gtatcatata	tgccaacatc	tgaggacag	720
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<210> 54
 <211> 759
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(759)
 <223> human metapneumovirus, strain Quebec Isolate No C-74501

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	acagggttgg	acaccaatgt	ctttacatta	gaagttgggtg	atgttgaaaa	tcttacatgt	180
	actgatggac	ctagcttaat	caaaacagaa	cttgacctaa	ccaaaagtgc	tctaagagaa	240
	ctcaaaacag	tttctgctga	tcagttagcg	agagaagaac	aaattgaaaa	tcccagacaa	300
	tcaagggttg	tcctaggtgc	aatagctctt	ggtgttgcca	cagcagcagc	agtcacagca	360
	ggcattgcga	tagccaaaac	cataaggctt	gagagtgaag	tgaatgcaat	caaagggtgct	420
	ctcaaaacaa	ccaacgaggc	agtatccaca	ctaggaaatg	gagtgcgagt	cctagccact	480
	gcagtaagag	agctgaaaga	atttgtgagc	aaaaacctga	ctagtgcatt	taacaagaac	540
	aaatgtgaca	ttgctgatct	gaagatggct	gtcagcttca	gtcaattcaa	cagaagattc	600
	ctaaatgttg	tgcggcagtt	ttcagacaat	gcagggataa	caccagcaat	atcatttagac	660
	ctaattgactg	atgctgagct	ggccagagct	gtatcatata	tgccaacatc	tgaggacag	720
	ataaaactaa	tgtrtagagaa	ccgtgcaatg	gtaagaaga			759

<210> 55
 <211> 759
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(759)
 <223> human metapneumovirus, strain Quebec Isolate No C-78429

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	acaggctggg	acattaatgt	cttcacatta	gaagttgggtg	atgttgaaaa	tcttacatgt	180
	actgatggac	ctagcttaat	caaaacagaa	cttgacctaa	caaaaagtgc	ttaaggggaa	240
	ctcaaaacag	tttctgctga	tcagttagcg	agagaggagc	aaattgaaaa	tcccagacaa	300
	tcaagatttg	tcctaggtgc	aatagctctc	ggagrtgcta	cagcagcagc	agtcacagca	360
	ggcattgcaa	tagccaaaac	cataaggctt	gagagtgaag	tgaatgcaat	taaagggtgct	420
	ctcaaaacaa	ctaattgaagc	agtatccaca	ttaggaaatg	gtgtgcgggt	cctagccact	480
	gcagtgagag	agctaaaaga	atttgtgagc	aaaaatctga	ctagtgcatt	caacaggaac	540
	aaatgtgaca	ttgctgatct	gaagatggct	gtcagcttca	gtcaattcaa	cagaagattt	600
	ctcaatgttg	tgcggcagtt	ttcagacaat	gcagggataa	caccagcaat	atcattggac	660
	ctaattgactg	atgctgaatt	ggccagagct	gtatcatata	tgccaacatc	tgaggacag	720
	ataaaactga	tgtrtgagaa	ccgtgcaatg	gtaagaaga			759

<210> 56
 <211> 759
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(759)
 <223> human metapneumovirus, strain Quebec Isolate No C-78652

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<400> 56
atgtccttga aagtgggtgat catcatttcg ttactcataa caccacagca cgggctaaag 60
gagagttatt tggagaatc atgcagtact ataactgagg gatacctcag tgttttaaga 120
acgggctggg acactaatgt cttcacatta gaagttgggt atgttgaaaa tcttacatgt 180
actgatggac ctactttaat caaaacagaa cttgacctaa caaaaagtgc tctaagggaa 240
ctcaaaacag tctctgctga tcagtttaacg agagaaggagc aaattgaaaa tcccagacaa 300
tcaagatttg tcttaggtgc aatagctctc ggagttgcta cagcagcagc agtcacagca 360
ggcattgcaa tagccaaaac cataaggcctt gagagtggag tgaatgcaat taaagggtgt 420
ctcaaaacaa ctaatgaagc agtatccaca ttaggaaatg gtgtgagggt cctagccact 480
gcagtgagag agctaaaaga atttgtgagc aaaaatctga ctagtgcatt caacagggaac 540
aaatgtgaca ttgtgatctt gaagatggct gtcagcttca gtcaattcaa cagaagattt 600
ctaaatgttg tgcggcagtt ttccagacaat gcagggataa caccagcaat atcattggac 660
ctaattgactg atgctgaatt ggccagagct gtatcatata tgccaacatc tgcaggacag 720
ataaaactga tgttgagaa ccgtgcaatg gtaagaaga 759

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<210> 57
<211> 759
<212> DNA
<213> human metapneumovirus

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```

<220>
<221> gene
<222> (1)...(759)
<223> human metapneumovirus, strain Quebec Isolate No
hMPV-118

```

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<400> 57
atgtccttga aaggggtgat tatcatttcg ttactcataa cacctcagca cggactaaaa 60
gaaagttatt tagaagaatc atgtagtact ataactgaag gatatctcag tgttttaaga 120
acaggttggg acaccaatgt ctttacatta gaagttgggt atgttgaaaa tcttacatgt 180
actgatggac ctactttaat caaaacagaa cttgacctaa ccaaaagtgc tctgagagaa 240
ctcaaaacag tttctgctga tcagtttaacg agagaagaac aaattgaaaa tcccagacaa 300
tcaaggtttg tcttaggtgc aatagctctt ggtgttgcca cagcagcagc agtcacagca 360
ggcattgcaa tagccaaaac cataaggcctt gagagtgaag tgaatgcaat caaagggtgt 420
ctcaaaacaa ccaacgaggc agtatccaca ctaggaaaatg gagtgcgagt cctagccacc 480
gcagtaagag agctgaaaga atttgtgagc aaaaacctga ccagtgcatt taacaagaac 540
aaatgtgaca ttgtgatctt gaagatggct gtcagcttca gtcaattcaa cagaagattc 600
ctaaatgttg tgcggcagtt ttccagacaat gcagggataa caccagcaat atcattagac 660
ctaattgactg atgctgagct ggccagagct gtatcatata tgccaacatc tgcaggggcag 720
ataaaactaa tgttagagaa ccgtgcaatg gtaagaaga 759

```

```

<210> 58
<211> 759
<212> DNA
<213> human metapneumovirus

```

```

<220>
<221> gene
<222> (1)...(759)
<223> human metapneumovirus, strain Quebec Isolate No
hMPV-200

```

```

<400> 58
atgtccttga aagtgggtgat cattttttcg ttactcataa cacctcagca cggactaaaa 60
gaaagttatt tagaagaatc atgtagtact ataactgaag gatatctcag tgttttaaga 120
acaggttggg acaccaatgt ctttacatta gaagttgggt atgttgaaaa tcttacatgt 180
actgatggac ctactttaat caaaacagaa cttgacctaa ccaaaagtgc tctaagagaa 240
ctcaaaacag tttctgctga tcagtttaacg agagaagaac aaattgaaaa tcccagacaa 300
tcaaggtttg tcttaggtgc aatagctctt ggtgttgcca cagcagcagc agtcacagca 360
ggcattgcaa tagccaaaac cataaggcctt gagagtgaag tgaatgcaat caaagggtgt 420
ctcaaaacaa ccaacgaggc agtatccaca ctaggaaaatg gagtgcgagt cctagccacc 480
gcagtaagag agctgaaaga atttgtgagc aaaaacctga ccagtgcatt taacaagaac 540
aaatgtgaca ttgtgatctt gaagatggct gtcagcttca gtcaattcaa cagaagattc 600
ctaaatgttg tgcggcagtt ttccagacaat gcagggataa caccagcaat atcattagac 660
ctaattgactg atgctgagct ggccagagct gtatcatata tgccaacatc tgcaggggcag 720
ataaaactaa tgttagagaa ccgtgcaatg gtaagaaga 759

```

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<210> 59
<211> 759
<212> DNA
<213> human metapneumovirus

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<220>
 <221> gene
 <222> (1)...(759)
 <223> human metapneumovirus, strain Quebec Isolate No
 hMPV-176

<400> 59
 atgtccttggg aagtgggtgat tatcatttgc ttactcataa cacctcagca cggactaaaa 60
 gaaagtatt tagaagaatc atgtagtact ataactgaag gatattctag tgttctaaga 120
 acagggttgg acaccaatgt ctttacatta gaagtgggtg atgttgaaaa tcttacatgt 180
 actgatggac ctatgttaac caaacacagaa cttgacctaa ccaaaagtgc ttttaagagaa 240
 ctcaaaacag tttctgctga tcagttagcg agagaagaac aaattgaaa tcccagacaa 300
 tcaagggtttg tcctagggtgc aatagctctc ggagttgcca cagcagcagc agtcacagca 360
 ggcattgcaa tagccaaaac tataagggtt gagagtgaag tgaatgcaat caaagggtgct 420
 ctcaaaacaa ccaatgaggc agtatcaaca ctaggaaatg gagtgccgtt cctagccact 480
 gcagtaagag agctgaaaga atttgtgagc aaaaacctga ctagtgcgat caacaagaac 540
 aaatgtgaca ttgtcgattt gaagatggct gtcagcttca gtcagttcaa cagaagattc 600
 ctaaaatgttg tgcggcagtt ttcaagacaat gcagggataa caccagcaat atcattggac 660
 ctgatgactg atgctgagct ggccagagct gtatcataca tgccaacatc tgcaggacag 720
 ataaaactaa tgrtagagaa ccgtgcaatg gtaagaaga 759

<210> 60
 <211> 711
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(711)
 <223> human metapneumovirus, strain Quebec Isolate No
 hMPV-193

<400> 60
 atggagggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtgaaaaat 60
 cgtgtggcac gcagcaaatg ctttaaaaaat gcctctttga tcctaataagg aataactaca 120
 ttgagtatag cctcaatat ctatctgac ataaactata caatgcaaga aaacacatcc 180
 gaatcagaac atcacaccag ctcatcacc atggaatcca gcagggaac tccaacggtc 240
 cccatggact acccagacac caatccaggc tcacagtatc caactcaaca gtccacagaa 300
 ggctccacac tctactttgc agcctcagca agctcaccag agacagaacc aacatcaaca 360
 ccaaacacaa caagccgccc gcccttcgtc gacacacaca caacaccacc aagtgcaggc 420
 agaacaaaga caagtccggc agtccacaca aaaaacaatc caaggataag cctcagaaca 480
 cattccccac catgggcaat gacaaggacg gtccgcgga ccaccactct ccgcacaagc 540
 agcacaagaa aaagaccgtc tacagcatca gtccaaactg acagcagcgc aacaaccac 600
 aaacacgaag aagcaagccc agtgagcccc caaacatctg caagcacagc aagaccacaa 660
 aggaagggtca tggaggccag cacatcaaca acatacaatc aaactagtta a 711

<210> 61
 <211> 711
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(711)
 <223> human metapneumovirus, strain Quebec Isolate No
 hMPV-228

<400> 61
 atggagggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtgaaaaat 60
 cgtgtggcac gcagcaaatg ctttaaaaaat gcctctttga tcctaataagg aataactaca 120
 ttgagtatag cctcaatat ctatctgac ataaactata caatgcaaga aaacacatcc 180
 gaatcagaac atcacaccag ctcatcacc atggaatcca gcagggaac tccaacggtc 240
 cccatggact acccagacac caatccaggc tcacagtatc caactcaaca gtccacagaa 300
 ggctccacac tctactttgc agcctcagca agctcaccag agacagaacc aacatcaaca 360
 ccaaacacaa caagccgccc gcccttcgtc gacacacaca caacaccacc aagtgcaggc 420
 agaacaaaga caagtccggc agtccacaca aaaaacaatc caaggataag cctcagaaca 480
 cattccccac catgggcaat gacaaggacg gtccgcgga ccaccactct ccgcacaagc 540
 agcacaagaa aaagaccgtc tacagcatca gtccaaactg acagcagcgc aacaaccac 600
 aaacacgaag aagcaagccc agtgagcccc caaacatctg caagcacagc aagaccacaa 660
 aggaagggtca tggaggccag cacatcaaca acatacaatc aaactagtta a 711

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<210> 62
 <211> 711
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(711)
 <223> human metapneumovirus, strain Quebec Isolate No
 C-77748

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<400> 62
atggagggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtgaaaaat 60
cgtgtggcac gcagcaaatg ctttaaaaat gcctctttga tcctaatagg aataactaca 120
ttgagtatag ccttcaaat ctatctaata ataaactata caatgcaaga aaacacatcc 180
gaatcagaac atcacaccag ctcatcacc atggaatcca gcagggaac tccaacagtc 240
cctatggaca actcagacac caatccaggc tcacagtatc caactcaaca gtccacagaa 300
ggctccacac tctactttgc agcctcagca agctcaccag agacagaacc aacatcaaca 360
ccagacacaa caagccgccc gcccttcgtc gacacacaca caacaccacc aagtgcaggc 420
agaacaagga caagtccggc agtccacaca aaaaacaatc caaggacaag cccagaata 480
cattccccac catgggcaat gacaaggacg gtccgtggaa ccaccactct ccgcacaagc 540
agcacaagaa aaagaccgtc tacagcatca gtccaacctg acagcagcgc aacaaccac 600
aaacacgaag aagcaagccc agtgagcccg caaacatctg cgagcacagc aagaccacaa 660
aggaagggca tggaggccag cacatcaaca acatacaacc aaactagtta a 711
```

<210> 63
 <211> 711
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(711)
 <223> human metapneumovirus, strain Quebec Isolate No
 C-78132

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<400> 63
atggagggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtgaaaaat 60
cgtgtggcac gcagcaaatg ctttaaaaat gcctctttga tcctaatagg aataactaca 120
ttgagtatag ccttcaaat ctatctgatc ataaactata caatgcaaga aaacacatcc 180
gaatcagaac atcacaccag ctcatcacc atggaatcca gcagggaac tccaacggtc 240
cctatagaca actcagacac caatccaggc tcacagtatc caactcaaca gtccacagaa 300
ggctccacac tccactttgc agcctcagca agctcaccag agacagaacc aacatcaaca 360
ccagacacaa caagccgccc gcccttcgtc gacacacaca caacaccacc aagtgcaggc 420
agaacaagga caagtccggc agtccacaca aaaaacaatc taaagataag cccagaata 480
cattccccac catgggcaat gacaaggacg gtccgtggaa ccaccactct ccgcacaagc 540
agcacaagaa aaagaccgtc tacagcatca gtccaacctg acagcagcac aacaactcac 600
aaacacgaag aagcaagccc agtgagcccg caaacatctg caagcacagc aagaccacaa 660
aggaagggca tggaggccag cacatcaaca acatacaacc aaactagtta a 711
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<210> 64
 <211> 711
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(711)
 <223> human metapneumovirus, strain Quebec Isolate No
 C-78406

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<400> 64
atggagggtga aagtggagaa cattcgaaca atagatatgc tcaaagcaag agtgaaaaat 60
cgtgtggcac gcagcaaatg ctttaaaaat gcctctttga tcctaatagg aataactaca 120
ttgagtatag ccttcaaat ctatctgatc ataaactata caatgcaaga aaacacatcc 180
gaatcagaac atcacaccag ctcatcacc atggaatcca gcagggaac tccaacggtc 240
cctatagaca actcagacac caatccaggc tcacagtatc caactcaaca gtccacagaa 300
ggctccacac tccactttgc agcctcagca agctcaccag agacagaacc aacatcaaca 360
ccagacacaa caagccgccc gcccttcgtc gacacacaca caacaccacc aagtgcaggc 420
agaacaagga caagtccggc agtccacaca aaaaacaatc taaagataag cccagaata 480
cattccccac catgggcaat gacaaggacg gtccgtggaa ccaccactct ccgcacaagc 540
agcacaagaa aaagaccgtc tacagcatca gtccaacctg acagcagcac aacaactcac 600
```


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aaacacgaag	aagcaagccc	agtgagccca	caaacatctg	caagcacagc	aagaccacaa	660
aggaaggcca	tggaaggccag	cacatcaaca	acatacaacc	aaactagtta	a	711

<210> 65
 <211> 711
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(711)
 <223> human metapneumovirus, strain Quebec Isolate No C-73750

<400> 65	atggagggtga	aagtggagaa	cattcgaaca	atagatatgc	tcaaagcaag	agtgaataat	60
	cggtgtggcac	gcagcaaatg	ctttaaaaat	gcctctttga	tcctaataag	aataactaca	120
	ttgagtataag	ccctcaacat	ctatctgac	ataaactata	caatgcaaga	aaacacatcc	180
	gaatcagaac	atcacaccag	ctcatcacc	atggaatcca	gcagggaac	tccaacgggc	240
	cctatagaca	actcagacac	caatccaggc	tcacagratc	caactcaaca	gtccacagaa	300
	ggctccacac	tccactttgc	agcctcagca	agctcaccag	agacagaacc	aacatcaaca	360
	ccagacacaa	caagccgccc	gcccttcgtc	gacacacaca	caacaccacc	aagtgcaagc	420
	agaacaagga	caagtccggc	agtcacacac	aaaaacaatc	taaagataag	ccccagaaca	480
	cattccccac	catgggcaat	gacaaggacg	gtccgtggaa	ccaccactct	ccgcacaagc	540
	agcataagaa	aaagaccgtc	cacagcatca	gtcccaacctg	acagcagcac	aacaaccac	600
	aaacacgaag	aagcaagccc	agtgagccca	caaacatctg	caagcacagc	aagaccacaa	660
	aggaaggcca	tggaaggccag	cacatcaaca	acacacaacc	aaactagtta	a	711

<210> 66
 <211> 660
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(660)
 <223> human metapneumovirus, strain Quebec Isolate No C-60298

<400> 66	atggagggtga	aagtggagaa	cattcgaaca	atagatatgc	tcaaagcaag	agtgaataat	60
	cggtgtggcac	gcagcaaatg	ctttaaaaat	gcctctttga	tcctaataag	aataactaca	120
	ttgagtataag	ccctcaacat	ctatctgac	ataaactata	caatgcaaga	aaacacatcc	180
	gaatcagaac	atcacaccag	ctcatcacc	atggaatcca	gcagggaac	tccaacgggc	240
	tccacagaca	accagacat	caatccaggc	tcacagratc	caactcaaca	gtccacagaa	300
	aacccccac	tcaacccgc	agcatcagtg	agcccatcag	aaacagaacc	agcatcaaca	360
	ccagacacaa	caaacccgct	gtcctccgta	gacaggtcca	cagcacaacc	aagtgaagc	420
	agaacaaga	caaacccgac	agtcacacac	agaaacaacc	caagcacagc	ttccagta	480
	caatccccac	cacgggcaac	aacgaaggca	atccgcagag	ccaccacttt	ccgcataagc	540
	agcacaggaa	aaagaccgtc	cacacacatca	gtccagtcg	acagcagcac	cacaaccac	600
	aatcatgaag	aaacagggttc	agcgaaccca	caggcatctg	taagcacaat	gcaaaactag	660

<210> 67
 <211> 654
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(654)
 <223> human metapneumovirus, strain Quebec Isolate No C-74783

<400> 67	atggagggtga	aagtggagaa	cattcgaaca	atagatatgc	tcaaagcaag	agtgaataat	60
	cggtgtggcac	gcagcaaatg	ctttaaaaat	gcctctttga	tcctaataag	aataactaca	120
	ttgagtataag	ccctcaacat	ctatctgac	ataaaccaca	caatacaaaa	aaccacatct	180
	gaatcagaac	accacaccag	ctcaccacc	acagaatcca	acaagggaagc	ttcaacaatc	240
	tccacagaca	accagacat	caatccaaac	tcacagcatc	caactcaaca	gtctacagaa	300
	aacccccac	tcaacccgc	agtatcaaca	agcccatcag	aaacagaacc	aacatcaaca	360
	ccagacacaa	caaacccgct	gtcctccgta	gacaggtcca	cagcacaacc	aagtgaagc	420
	agaacaaga	caaatccgac	agtcacacac	agaaacaacc	caagcacagc	ttccagta	480

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caatccccac	cacggggcaac	aacgaaggca	atccgcagag	ccaccacttt	ccgcatgagc	540
agcacagaaa	aaagaccaac	cacaacacta	gtccagtacg	acagcagcac	cacaacccaa	600
aatcatgaag	aaacagggtt	agcgaaccca	caggcatctg	caagcacaat	gtaa	654

<210> 68
 <211> 660
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(660)
 <223> human metapneumovirus, strain Quebec Isolate No C-74549

<400> 68						
atggagggtga	aagtggagaa	cattcgagca	atagacatgc	tcaaagcaag	agtgaaaaat	60
cgtgtggcac	gtagcaaatg	cttcaaaaat	gcttcccaa	tcctcacagg	aataaccaca	120
ctgagcatag	ctctcaatat	ccacctgac	ataaactaca	caatacaaaa	aaccacatct	180
gaatcagaac	accacaccag	ctcaccaccc	acagaatcta	acaaggaagc	ttcaacaatc	240
tccacagaca	accacagacat	caatccaac	tcacagcatc	caactcaaca	gtctacagaa	300
aacccacac	tcaaccccg	agtatcaaca	agcccatcag	aaacagaacc	aacatcaaca	360
ccagacacaa	caaacgcct	gtctccgta	gacaggtcca	cagcacaacc	aagtgaagc	420
agaacaaaga	caaaatcgat	agtccacaca	agaaacaacc	caagcacagc	ttccagcaca	480
caatccccac	cacggggcaac	aacgaaggca	atccgcagag	ccaccacttt	ccgcatgagc	540
agcacagaaa	aaagaccaac	cacaacatta	gtccagtacg	acagcagcac	cacaacccaa	600
aatcatgaag	aaacagggtt	agcgaaccca	caggcatctg	taagcacaat	gtaaaactag	660

<210> 69
 <211> 711
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(711)
 <223> human metapneumovirus, strain Quebec Isolate No C-77807

<400> 69						
atggagggtga	aagtggagaa	cattcgaaca	atagatatgc	tcaaagcaag	agtgaaaaat	60
cgtgtggcac	gcagcaaatg	cttcaaaaat	gcttctttga	tcctaataagg	aataacgaca	120
ttgagtatag	ccctcaacat	ctatctgac	ataaactata	caatgcaaga	aaacacatcc	180
gaatcagaac	atcacaccag	ctcatcacc	atggaatcca	gcagggaaac	tccaacggtc	240
cctatagaca	actcagacac	caatccaggc	tcacagtatc	caactcaaca	gtccacagaa	300
ggctccacac	tccactttgc	agcctcagca	agctcaccag	agacagaacc	aacatcaaca	360
ccagacacaa	caagccgccc	gcccttcgtr	gacacacaca	caacaccacc	aagtgaagc	420
agaacaagga	caagtccggc	agtccacaca	aaaaacaatc	taagataaag	ccccagaata	480
caatccccac	catgggcaat	gacaaggacg	gtccgtggaa	ccaccactct	ccgcacaagc	540
agcacagaag	aaagaccgtc	tacagcatca	gtccaacctg	acagcagcac	aacaactcac	600
aaacacgaag	aagcaagccc	agtgagccca	caaactctg	caagcacagc	aagaccacaa	660
aggaagggtga	tggaggccag	cacatcaaca	acatacaacc	aaactagtta	a	711

<210> 70
 <211> 711
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(711)
 <223> human metapneumovirus, strain Quebec Isolate No C-78163

<400> 70						
atggagggtga	aagtggagaa	cattcgaaca	atagatatgc	tcaaagcaag	agtgaaaaat	60
cgtgtggcac	gcagcaaatg	cttcaaaaat	gcttctttga	tcctaataagg	aataactaca	120
ttgagtatag	ccctcaacat	ctatctgac	ataaactata	caatgcaaga	aaacacatcc	180
gaatcagaac	atcacaccag	ctcatcacc	atggaatcca	gcagggaaac	tccaacggtc	240
cctatagaca	actcagacac	caatccaggc	tcacagtatc	caactcaaca	gtccacagaa	300
ggctccacac	tccactttgc	agcctcagca	agctcaccag	agacagaacc	aacatcaaca	360
ccagacacaa	caagccgccc	gcccttcgtr	gacacacaca	caacaccacc	aagtgaagc	420

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agaacaagga	caagtccggc	agtccacaca	aaaaacaatc	taaagataag	ccccagaata	480
cattcccccac	catggggcaat	gacaaggacg	gtccgtggaa	ccaccactct	ccgcacaagc	540
agcacaagaa	aaagaccgct	tacagcatca	gtccaaacctg	acagcagcac	aacaactcac	600
aaacacgaag	aagcaagccc	agtgaagccc	caaacatctg	caagcacagc	aagaccacaa	660
aggaagggca	tggaggccag	cacatcaaca	acatacaacc	aaactagtta	a	711

<210> 71
 <211> 711
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(711)
 <223> human metapneumovirus, strain Quebec Isolate No C-68661

<400> 71						
atggagggtga	aagtggagaa	cattcgaaca	atagatagcg	tcaaagcaag	agtgaaaaat	60
cgtgtggcac	gcagcaaatg	ctttaaaaat	gcctctttga	tcctaataagg	aataactaca	120
ttgagttag	ccctcaatat	ctatctgac	ataaactata	caatgcaaga	aaacacatcc	180
aaatcagaac	atcacaccag	ctcatcacc	atggaatcca	gcagggaaac	tccaacggtc	240
cctatagaca	actcagacac	caatccaggc	tcacagtatc	caactcaaca	gtccacagaa	300
ggctccacac	tccactttgc	agcctcagca	agctcaccag	agacagaacc	aacatcaaca	360
ccagacacaa	caagccgccc	gcccttcgtc	gacacacaca	caacaccacc	aagtgcgaagc	420
agaacaagga	caagtccggc	agtccacaca	aaaaacaatc	caaggataag	ccccagaaca	480
cattcccccac	catggggcaat	gacaaggacg	gtccgtggaa	ccaccactct	ccgcacaagc	540
agcacaagaa	aaagaccgct	cacagcatca	gtccaaacctg	acagcagcgc	aacaaccac	600
aaacacgaag	aagcaagccc	agtgaagccc	caaacatctg	caagcacagc	aagaccacaa	660
aggaagggca	tggaggccag	cacatcaaca	acatacaacc	aaactagtta	a	711

<210> 72
 <211> 711
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(711)
 <223> human metapneumovirus, strain Quebec Isolate No C-88448

<400> 72						
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gaatcagaac	atcacaccag	ctcatcacc	atggaatcca	gcagggaaac	tccaacagtc	240
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ggctccacac	tctactttgc	agcctcagca	agctcaccag	agacagaacc	aacatcaaca	360
ccagacacaa	caagccgccc	gcccttcgtc	gacacacaca	caacaccacc	aagtgcgaagc	420
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cattcccccac	catggggcaat	gacaaggacg	gtccgtggaa	ccaccactct	ccgcacaagc	540
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aaacacgaag	aagcaagccc	agtgaagccc	caaacatctg	cgagcacagc	aagaccacaa	660
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<210> 73
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 <212> DNA
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<220>
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 <223> human metapneumovirus, strain Quebec Isolate No C-88470

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ttgagttag	ccctcaatat	ctatctgac	ataaactata	caatgcaaga	aaacacatcc	180
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aaacacgaag aagcaagccc agtgagcccc caaacatctg caagcacagc aagaccacaa 660
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<220>
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gaatcagaac atcacaccag ctcatcacc atggaatcca gcaaggaaac tccaacagtc 240
cctatggaca actcagacac caatccaggc tcacagtatc caactcaaca gtccacagaa 300
ggctccacac tctactttgc agcctcagca agctcaccag agacagaacc aacatcaaca 360
ccagacacaa caagccgccc gcccttcgtc gacacacaca caacaccacc aagtgcgaagc 420
agaacaagga caagtccggc agtccacaca aaaaaaatc caaggacaag cctcagaaca 480
cattccccac catgggcaat gacaaggacg gtccgtggaa ccaccactct ccgcacaagc 540
agcacaaaga aaagaccgtc cacagcatca gtccaacctg acagcagcgc aacaacccac 600
aaacacgaag aagcaagccc agtgagcccc caaacatctg cgagcacagc aagaccacaa 660
aggaagggtca tggaggccag cacatcaaca acatacaacc aaactagtta a 711

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<210> 75
 <211> 6017
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(6017)
 <223> human metapneumovirus, strain 00-1
 accession number af371337

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aaaaaatgaca acactgcaaa agttgccata gagaatctctg ttatcgagca ttttagactc 180
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atgcaacatg aaattatgaa gaattgtacac agttgtgagc tcacattatt aaaacagttt 300
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ttaaagtcta catcagatga tacctcaatc ctaagtttta tagatgtaga atttatacct 420
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cttaggatta ctgaacatgc tcaattcagt actagattta gaaatacttt attaaatgga 900
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taacaaacaa	ggcaaacaca	ataattgatt	ggttagaaca	tattttaaat	tctccaaaag	5880

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 taatagataa tctagggaat gcagagataa aaaaactgat caaagtaact ggatatatgc 6000
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<211> 450

<212> DNA

<213> human metapneumovirus

<220>

<221> gene

<222> (1)...(450)

<223> human metapneumovirus, strain Quebec Isolate No
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 aagaaccggt tcaatcttgt gcaggtcatt aggtaaatta gtttttattg tatcatcata 360
 tggatgtatc gtcaagagca acaaaagcaa aagagtgtgc ttctttacat acaatcaact 420
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<210> 77

<211> 450

<212> DNA

<213> human metapneumovirus

<220>

<221> gene

<222> (1)...(450)

<223> human metapneumovirus, strain Quebec Isolate No
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 gtatagtcga gagcaacaaa agcaaaagag tgagcttctt cacatacaat caactgttaa 420
 catggaaaga tgtgatgtta agtagattca 450

<210> 78

<211> 500

<212> DNA

<213> human metapneumovirus

<220>

<221> gene

<222> (1)...(500)

<223> human metapneumovirus, strain Quebec Isolate No
hMPV-174

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 tacaatctca acaagttagt tctggaaattc aggaagaag aagtaataag aactggttca 360
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 aagagcaaca aaagcaaaag agtgagcttc ttcacataca atcaactgtt aacatggaaa 480
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<210> 79

<211> 450

<212> DNA

<213> human metapneumovirus

<220>

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<221> gene
 <222> (1)...(450)
 <223> human metapneumovirus, strain Quebec Isolate No
 hmpv-184

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<210> 80
 <211> 500
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(500)
 <223> human metapneumovirus, strain Quebec Isolate No
 hmpv-196

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 agcactctca aattaaatat gatattgtgat tggctgcaat taaagtctac atcagatgat 240
 acctcaatcc taagtttcat agatgtagaa ttatataccta gttgggtaag caactgggtt 300
 agtaattggt acaatctcaa taagttaatt ttggaattca gaagagaaga agtaataaga 360
 accggttcaa tcttatgcag gtcattgggt aaattagttt ttattgtatc atcatatgga 420
 tgtatcgtca agagcaacaa aagcaaaaaga gtgagcttct tcacatacaa tcaactgtta 480
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<210> 81
 <211> 450
 <212> DNA
 <213> human metapneumovirus

<220>
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 <222> (1)...(450)
 <223> human metapneumovirus, strain Quebec Isolate No
 C-76837

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 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(450)
 <223> human metapneumovirus, strain Quebec Isolate No
 C-77807

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 gaagaatgta cacagttgtg agctcacatt attaaaaacag tttttaacaa ggagtaaaaa 120

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<210> 83
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 <221> gene
 <222> (1)...(450)
 <223> human metapneumovirus, strain Quebec Isolate No
 hmpv-185

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aagaaccggg	tcaatcttat	gcaggtcatt	gggtaaatta	gtttttattg	tatcatcata	360
tggtatgtatc	gtcaagagca	acaaaagcaa	aagagtggagc	ttcttcacat	acaatcaact	420
gttaacatgg	aaagatgtga	tgtaagtag				450

<210> 84
 <211> 500
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(500)
 <223> human metapneumovirus, strain Quebec Isolate No
 C-78123

<400> 84						
atcctgttat	cgagcatgtt	agactcaaaa	atgcaatcaa	ttctaagatg	aaaatatcag	60
attacaggat	agtagagcca	gtaaacatgc	aacatgaaat	tatgaagaat	gtacacagtt	120
gtagctcac	attattaaaa	cagtttttaa	caaggagtaa	aaatattagc	actctcaaat	180
taaaatgatg	atgtgattgg	ctacagttaa	agctctacatc	agatgatacc	tcaatcttaa	240
gttttataga	tgtagaattt	atacctagct	gggtaagcaa	ttggtttagt	aattggtaaa	300
atctcaacaa	gttgattctg	gaattcagga	aagaagaagt	aataagaact	ggttcaatct	360
tgtagaggtc	tttgggtaaa	ttagtttttg	ttgtatcatc	atatggatgt	atagtcaga	420
gcaacaaaag	caaaaagagt	agcttcttca	catacaatca	actgttaaca	tggaaagatg	480
tgatgttaag	tagattcaat					500

<210> 85
 <211> 450
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(450)
 <223> human metapneumovirus, strain Quebec Isolate No
 C-91205

<400> 85						
caatttctaaa	atgaaaatat	cagattacaa	ggtagtagag	ccagtaaaaca	tgcaacatga	60
aataatgaag	aatgtacaca	gttgtgagct	cacactattg	aaacagtttt	taacaaggag	120
taaaaacatt	agcactctca	aattaaatat	gatatgtgat	tggctgcaat	taaagtctac	180
atcagatgat	acctcaatcc	taagtttcat	agatgtagaa	tttataccta	gttgggtaag	240
caactgggtt	agtaattggg	acaatctcaa	taagtttaatt	ttgggaattca	gaagagaaga	300
agtaataaga	accgggtcaa	tcttatgcag	gtcattgggt	aaattagttt	ttattgtatc	360
atcatatgga	tgtattgtca	agagcaacaa	aagcaaaaaga	gtgagcttct	tcacatacaa	420
tcaactgita	acatggaaa	atgtgatgtt				450

<210> 86

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<211> 400
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(400)
 <223> human metapneumovirus, strain Quebec Isolate No
 C-91364

<400> 86
 ttgcatagag aatcctgtta ttgagcatgt cagactcaaa aatggcagta attctaaaat 60
 gaaaatatca gattacaagg tagtagaacc agtaaaccatg caacatgaaa taatgaagaa 120
 tgtacacagc tgtgagcaca cactattgaa acagttttta acaaggagta aaaacattag 180
 cactctcaaa ttaaatatga tatgtgattg gctgcaatta aaatctacat cagatgggtac 240
 ctcaatccta agttttatag atgtagaatt tacccttagt tgggtaagca actgggttag 300
 taattggcac aatctcaata agttaatttt agaattcagg agagaagaag taataagaac 360
 cggttcaatc ttgtgcagggt cattaggttaa attagttttt 400

<210> 87
 <211> 500
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(500)
 <223> human metapneumovirus, strain Quebec Isolate No
 C-91749

<400> 87
 atagagaatc ctggtattga gcatgtgaga ctcaaaaatg cagtcaattc taaaatgaaa 60
 atatcagatt acaaggtagt agagccagta aacatgcaac atgaaataat gaagaatgta 120
 cacagttgtg agctcacact attgaaacag tttttaacta ggagtaaaaa cattagcact 180
 ctcaaatata atattgatag tgattggctg caattaaagt ctacatcaga tgataacctca 240
 atcctaagtt tcatagatgt agaatttata cctagttggg taagcaactg gtttagtaat 300
 tgggtacaatc tcaataagtt aattttggaa ttcagaagag aagaagtaat aagaaccggt 360
 tcaatctttt gcaggtcatt gggtaaatta gtttttatg tatcatcata tggatgtatc 420
 gtcaagagca acaaaagcaa aagagtggagc ttcttcacat acaatcaact gttaacatgg 480
 aaagatgtga tgttaagtng 500

<210> 88
 <211> 450
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(450)
 <223> human metapneumovirus, strain Quebec Isolate No
 hmpv-Q86

<400> 88
 aattctaaaa tggaaatatc agattacaag gtagtagaac caataaacat gcaacatgaa 60
 ataataaga atgtacacag ttgtgagctc acactattga aacagttttt aacaaggagt 120
 aaaaacatta gcactctcaa attaaatatg atattgtgatt ggctgcaatt aaaatctaca 180
 tcagatgata cctcaatcct aagttttata gatgtagaat ttatacctag ttgggtaagc 240
 aactgggtta gtaattggta caatctcaat aagttaattt tagaattcag gagagaggaa 300
 gtaataagaa ccgggttcaat cttgtgcagg tcattaggta aattagtttt tattgtatca 360
 tcatatggat gtatcgtcaa gagcaacaaa agcaaaagag tgagcttctt cacatacaat 420
 caactgttaa catggaaaga tgtgatgtta 450

<210> 89
 <211> 450
 <212> DNA
 <213> human metapneumovirus

<220>
 <221> gene
 <222> (1)...(450)
 <223> human metapneumovirus, strain Quebec Isolate No
 hmpv-Q97

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```

<400> 89
aaaatgaaaa tadcagatta caaggtagta gagccagtaa acatgcaaca tgaaataatg    60
aagaatgtac acagttgtga gctcacacta ttgaaacagt ttttaactag gagtaaaaac    120
attagcactc tcaaattaaa tatgatattg gattggctgc aattaaagtc tacatcagat    180
gataacctca tcctaagttt catagatgta gaattttatc ctagtgggtg aagcaactgg    240
tttagtaatt ggtacaattt caataagtta attttggaaat tcagaagaga agaagtaata    300
agaaccgggt caatcttatg cagggtcattg ggtaaattag tttttattgt atcatcatat    360
ggatgtatcg tcaagagcaa caaaagcaaa agagttagct tcttcacata caatcaactg    420
ttaacatgga aagatgtgat gttaagtaga

```

```

<210> 90
<211> 537
<212> DNA
<213> human metapneumovirus

```

```

<220>
<221> gene
<222> (1)...(537)
<223> human metapneumovirus, strain Can 97-83

```

```

<400> 90
agaatcctgt tattgagcat gtgagactca aaaatggcgg tcattctaaa atgaaaatat    60
cagattacaa ggtagtagag ccagtaaaaca tgcaacatga aataatgaag aatgtacaca    120
gttgtagact cacactattg aaacagtttt taacaaggag taaaaacatt agcactctca    180
aattgaatat gatattgat tggctgcaat taaagtctac atcagatgat acctcaatcc    240
taagtttcat agatgtagaa ttctaccta gttgggttaag caactgggtt agtaattgggt    300
acaatctcaa taagttaatt ttggaattca gaagagagga agtaataaga accggttcaa    360
tcttatgcag gtcattgggt aaattagttt ttattgtatc atcatatgga tgtatcgta    420
agagcaacaa aagcaaaaaga gtgagcttct tcacatacaa tcaactgtta acatggaaaag    480
atgtgatgtt aagtagattt aatgcgaatt tttgtatatg ggtaagcaac agttcttg    537

```

```

<210> 91
<211> 20
<212> DNA
<213> human metapneumovirus

```

```

<220>
<223> primer no 55

```

```

<400> 91
atgggacaag tgaaaatgtc    20

```

```

<210> 92
<211> 19
<212> DNA
<213> human metapneumovirus

```

```

<220>
<223> primer no 56

```

```

<400> 92
gagtctcagt acacaataa    19

```

```

<210> 93
<211> 18
<212> DNA
<213> human metapneumovirus

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<220>
<223> primer no 57

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<400> 93
gtcactgcag ttgttgta    18

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```

<210> 94
<211> 19
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<220>
<223> primer no 58

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<400> 94 jcatttccga gaacaacac	19
<210> 95 <211> 19 <212> DNA <213> human metapneumovirus	
<220> <223> primer no 18 multiplex assay	
<400> 95 gagtctcagt acacaataa	19
<210> 96 <211> 19 <212> DNA <213> human metapneumovirus	
<220> <223> primer no 19 multiplex assay	
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<220> <223> primer no 59	
<400> 97 atgtcttggg aagtgggtg	18
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<220> <223> primer no 60	
<400> 98 tcttcttacc attgcac	17
<210> 99 <211> 20 <212> DNA <213> human metapneumovirus	
<220> <223> primer no 61	
<400> 99 ctaattatgt ggtatgaagc	20
<210> 100 <211> 18 <212> DNA <213> human metapneumovirus	
<220> <223> primer no 62	
<400> 100 atggagtcct acctagta	18
<210> 101 <211> 19	

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<212> DNA
<213> human metapneumovirus

<220>
<223> primer no 63

<400> 101
aaggtgcttg gttgttatc

19

<210> 102
<211> 19
<212> DNA
<213> human metapneumovirus

<220>
<223> primer no 64

<400> 102
atgtcattcc ctgaaggaa

19

<210> 103
<211> 19
<212> DNA
<213> human metapneumovirus

<220>
<223> primer no 65

<400> 103
ttaactggta aatctcatc

19

<210> 104
<211> 19
<212> DNA
<213> human metapneumovirus

<220>
<223> primer no 66

<400> 104
catgggacaa gtagttatg

19

<210> 105
<211> 19
<212> DNA
<213> human metapneumovirus

<220>
<223> primer no 67

<400> 105
atggaggtga aagtggaga

19

<210> 106
<211> 19
<212> DNA
<213> human metapneumovirus

<220>
<223> primer no 68

<400> 106
ttaactagtt tggttgtat

19

<210> 107
<211> 19
<212> DNA
<213> human metapneumovirus

<220>
<223> primer no 69

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<400> 107
 ttagagtta tttgtatt 19
 <210> 108
 <211> 24
 <212> DNA
 <213> human metapneumovirus
 <220>
 <223> primer no 70
 <400> 108
 ggacaagtag ttatggaggt gaaa 24
 <210> 109
 <211> 28
 <212> DNA
 <213> human metapneumovirus
 <220>
 <223> primer no 71
 <400> 109
 ctctttaag atatgagta ggmagta 28
 <210> 110
 <211> 22
 <212> DNA
 <213> human metapneumovirus
 <220>
 <223> primer no 20 multiplex assay
 <400> 110
 gttgcatag agaactctgt ta 22
 <210> 111
 <211> 22
 <212> DNA
 <213> human metapneumovirus
 <220>
 <223> primer no 21 multiplex assay
 <400> 111
 cattcagact gttgcttacc ca 22
 <210> 112
 <211> 22
 <212> DNA
 <213> human metapneumovirus
 <220>
 <223> primer no 72
 <400> 112
 gttgcatag agaactctgt ta 22
 <210> 113
 <211> 22
 <212> DNA
 <213> human metapneumovirus
 <220>
 <223> primer no 73
 <400> 113
 cattcagact gttgcttacc ca . 22
 <210> 114
 <211> 27
 <212> DNA

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<213> human Metapneumovirus

<220>

<223> human Metapneumovirus
primer A1

<400> 114

ccaattacta aaccaattgc ttacca

27

<210> 115

<211> 21

<212> DNA

<213> human metapneumovirus

<220>

<223> probe no 74

<400> 115

gcaagcttat ggggccggtc a

21

<210> 116

<211> 25

<212> DNA

<213> human metapneumovirus

<220>

<223> probe no 75

<400> 116

acaatgctaa ggtggggggt cattg

25

<210> 117

<211> 23

<212> DNA

<213> human metapneumovirus

<220>

<223> probe no 76

<400> 117

gttctgagga caggttggtgta cac

23

<210> 118

<211> 23

<212> DNA

<213> human metapneumovirus

<220>

<223> probe no 77

<400> 118

aatgttttta cactggaggt agg

23

<210> 119

<211> 22

<212> DNA

<213> human metapneumovirus

<220>

<223> probe no 78

<400> 119

gttacaatac cagcattcat ca

22

<210> 120

<211> 25

<212> DNA

<213> human metapneumovirus

<220>

<223> probe no 79

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<400> 120 atcagtttca atcaaagaga gtgag	25
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<220> <223> probe no 80	
<400> 121 taaagcaagc aatcaaagtc atgga	25
<210> 122 <211> 25 <212> DNA <213> human metapneumovirus	
<220> <223> probe no 81	
<400> 122 cccattgaag aagaagagtc taccg	25
<210> 123 <211> 20 <212> DNA <213> human metapneumovirus	
<220> <223> probe no 82	
<400> 123 actcaagccc acagcatcca	20
<210> 124 <211> 23 <212> DNA <213> human metapneumovirus	
<220> <223> probe no 83	
<400> 124 ctcaacagtc cacagaaggc tcc	23
<210> 125 <211> 26 <212> DNA <213> human metapneumovirus	
<220> <223> probe no 84	
<400> 125 attggttag taattggtac aatctc	26
<210> 126 <211> 26 <212> DNA <213> human metapneumovirus	
<220> <223> probe no 85	
<400> 126 acaagtgat tctggaattc aggaaa	26
<210> 127 <211> 25 <212> DNA	

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<213> human Metapneumovirus

<220>

<223> human Metapneumovirus
probe A2

<400> 127

cgagcatggt agactcaaaa atgca

25

<210> 128

<211> 23

<212> DNA

<213> human metapneumovirus

<220>

<223> probe no 33 multiplex assay

<400> 128

atgtatccgt ccaagctgag tta

23

<210> 129

<211> 26

<212> DNA

<213> human metapneumovirus

<220>

<223> probe no 34 multiplex assay

<400> 129

attggttttag taattggtac aatctc

26

<210> 130

<211> 1027

<212> DNA

<213> human Influenza A virus

<220>

<221> gene

<222> (1)...(1027)

<223> human Influenza A virus
strain A/Hong Kong/1180/99(H3N2)
accession number af386771

<400> 130

agcaaaaagca	ggtagatatt	gaaagatgag	ccttctaccc	gaggtcgaaa	cgtatgttct	60
ctctatcggt	ccatcaggcc	ccctcaaac	cgaaatcgcg	cagagacttg	aagatgtcct	120
tgctgggaaa	aacacagatc	ttgaggctct	catggaatgg	ctaaagacaa	gaccaatcct	180
gtcaccctcg	actaaggggg	ttttaggggt	tgtgttcacg	ctcaccgtgc	ccagtgaagc	240
aggactgcag	cgtagacgct	ttgtccaaaa	tgccctcaat	gggaatgggg	atccaaataa	300
catggacaaa	gcagtttaac	tgtatagaaa	acttaagagg	gagataacat	tccatggggc	360
caaagaaata	gcactcagtt	attctgctgg	tgcaacttgc	agtgtcatgg	gcctcatata	420
caataggatg	ggggctgtta	ccactgaagt	ggcatttggc	ctggtatgtg	caacatgtga	480
acagattgct	gactcccagc	acagggtctc	taggcaaatg	gtggcaacaa	ccaatccatt	540
aataagacat	gagaacagaa	tggttttggc	cagcactaca	gctaaggcta	tggagcaaat	600
ggctggatca	agtgaagcgg	cagcggaggc	catggagatt	gctagtcagg	ccaggcaaat	660
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tcttcttgaa	aatttgcaga	cttatcagaa	acggatgggg	gtgcagatgc	aacgattcaa	780
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ttgatcgtct	ttttttcaaa	tgcatctatc	gactcttcaa	acacggcctt	aaaagagggc	900
cttctacgga	aggagtacct	gagtctatga	gggaagaata	tcgaaaggaa	cagcagaatg	960
ctttggatgc	tgaccacagt	cattttgtca	gcataaagti	ggagtaaaaa	actaccttgt	1020
ttctact						1027

<210> 131

<211> 987

<212> DNA

<213> human Influenza A virus

<220>

<221> gene

<222> (1)...(987)

<223> human Influenza A virus

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strain A/Charlottesville/31/95 (H1N1)
accession number af398876

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<400> 131
atgagtcttc taaccgaggt cgaacgtac gtctctctta tcgtcccgtc aggccccctc 60
aaagccgaga tcgcacagag acttgaagat gtctttgctg gaaagaacac cgatcttgag 120
gctctcatgg agtggctaaa gacaagaccg atcctgtcac ctctgactaa ggggatttta 180
ggatttgggt tcacgctcac cgtgcccgag gagcgaggac tgcagcgtag acgctttgtc 240
caaatgccc ttaatgggaa tggggatcca aataacatgg acagagcagt taaactgtat 300
agaaagctta agagggagat aacattccat ggggccaaag aaatagcact cagttattct 360
gctgggtcac ttgcccagtt tatgggcctc atatacaaca ggaatggggc tgtgaccacc 420
gaatcagcat ttggcctgat atgcgcaacc tgtgaacaga ttgctgactc ccagcataag 480
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actcatccta gctctagcac tggctctgaaa aatgatcttc ttgaaaattt gcaggcctat 720
cagaaacgaa tgggggtgca gatgcaacga ttcaagtgat cctctgtgtg ttgccgcaag 780
tatcatttgg attgtgcacc tgatattgtg gattattgat cgcccttttt tcaaatgcat 840
ttatcgtatc tttaaacacg gtctgaaaag agggccttct acggaaggag taccagagtc 900
tatgagggaa gaatatcgag aggaacagca gaatgctgtg gatgctgacg aaggtcattt 960
tgcagcata gagctggagt aaaaaaac
```

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<210> 132
<211> 1076
<212> DNA
<213> human Influenza B virus
```

```
<220>
<221> gene
<222> (1)...(1076)
<223> human Influenza B virus
strain B/Nagoya/20/99
```

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<400> 132
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aaagcagaaac tagcagaaaa attacactgt tggttcggtg ggaaagaatt tgacctagac 120
tctgctttgg aatggataaa aaacaaaaga tgcttaactg atatacaaaa agcactaatt 180
ggtgccccta tctgcttttt aaaacccaaa gaccaagaaa gaaaaagaag attcatcaca 240
gagcccttat cagggaatggg aacaacagca acaaaaaaga aaggcctgat tctagctgag 300
agaaaaatga gaagtgtgtg gagctttcat gaagcatttg aaatagcaga aggccatgaa 360
agctcagcgc tactatatgt tctcatgggtc atgtacctga accctggaaa ttattcaatg 420
caagtataaac taggaacgct ctgtgctttg tgcgagaaac aagcatcaca ttcacacag 480
gctcatagca gagcagcgag atcttcagtg cctggagtga ggcgagaaat gcaaatgggtc 540
tcagctatga acacagcaaa aacaatgaat ggaatgggaa agggagaaga cgtccaaaaa 600
ctggcagaag aactgcaaa caacattgga gtgttgagat ctcttgagac aagtcaaaag 660
aatggggaaag gaattgcaaa ggatgtaatg gaagtgtctaa agcagagctc tatgggaaat 720
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aagtatcaat tttgagacac aattaccaaa aagaaatcca ggccaagaa acaatgaagg 960
aagtgtcttc tgacaacata gaagtattga gtgaccacat agtgattgag gggctttctg 1020
ctgaagagat aataaaaaatg ggcaaaacag ttttggagggt agaaaaattg cattraa 1076
```

```
<210> 133
<211> 1725
<212> DNA
<213> human Respiratory Syncytial Virus
```

```
<220>
<221> gene
<222> (1)...(1725)
<223> human Respiratory Syncytial Virus
strain B1
accession number af013254
```

```
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atggagctgc tgatccacag gttaagtgc atcttcttaa ctcttgctat taatgcattg 60
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agcagaggtt attttagtgc tttagaaca ggttgggtata ccagtgctcat aacaatagaa 180
ttaagtaata taaaagaaac caaatgcaat ggaactgaca ctaaagtata acttataaaa 240
caagaattag ataatgataa gaatgcagtg acagaattac agtactttat gcaaaacaca 300
ccagctgcca acaaccgggc cagaagagaa gcaccacagt atatgaacta tacaatcaat 360
```

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accactaaaa	acctaaatgt	atcaataaagc	aagaagagga	aacgaagatt	tctgggcttc	420
ttgttaggtg	taggatctgc	aatagcaagt	ggtatagctg	tatccaaagt	tctacacctt	480
gaaggagaag	tgaacaagat	caaaaatgct	ttgttatcta	caaacaagc	tgtagtcagt	540
ctatcaaatg	gggtcagtgt	tttaaccagc	aaagtgttag	atctcaagaa	ttacataaat	600
aaccaartat	taccatagat	aaatcaacag	agctgtcgca	tctccaacat	tgaaacagtt	660
atagaartcc	agcagaagaa	cagcagattg	ttggaaatca	acagagaatt	cagtgtcaat	720
gcaggtgtta	caacaccttt	aagcacttac	atgttaacaa	acagttagtt	actatcattg	780
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gtacagctac	ctatctatgg	tgtaatatag	acaccttgct	ggaaattaca	cacatcacct	960
ctatgcacca	ccaacatcaa	agaaggatca	aatatttggt	taacaaggac	tgatagagga	1020
tggtattgtg	ataatgcagg	atcagtatcc	ttctttccac	aggctgacac	ttgtaaagta	1080
cagtcgaatc	gagtatcttg	tgacactatg	aacagtttga	cattaccaag	tgaagtcagc	1140
ctttgttaaca	ctgcacatatt	caattccaag	tatgactgca	aaattatgac	atcaaaaaa	1200
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<210> 134

<211> 1575

<212> DNA

<213> human Parainfluenza 1 virus

<220>

<221> gene

<222> (1)...(1575)

<223> human Parainfluenza 1 virus strain
 washington/1964
 accession number nc003461

<400> 134

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<210> 135

<211> 1548

<212> DNA

<213> human Parainfluenza 3 virus

<220>

<221> gene

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<222> (1)...(1548)

<223> human Parainfluenza 3 virus
strain GP
accession number ab012132

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<210> 136

<211> 2910

<212> DNA

<213> human Adenovirus

<220>

<221> gene

<222> (1)...(2910)

<223> human Adenovirus
strain 105
accession number aj293903

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 <212> DNA
 <213> human Enterovirus

<220>
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 <222> (1)...(810)
 <223> human Enterovirus
 strain Coxsackievirus B1
 accession number M16560

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caaccgacg	tggccacatg	tcgggtctac	actttagagt	ccgtgcagtg	gatgaagaat	720
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<210> 138
 <211> 681
 <212> DNA
 <213> human Rhinovirus

<220>
 <221> gene
 <222> (1)...(681)
 <223> human Rhinovirus
 strain 14
 accession number K02121

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acagcatata	tatacatata	ctgtgatcat	gggcgctcag	gtttctacac	agaaaagtgg	180
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ttactataag	gatgcagcaa	gtacatcatc	agctgggtcaa	tcactgtcaa	tggaccctac	300
taagtgttaca	gaaccagtta	aagatctcat	gcttaagggt	gcaccagcat	tgaattcacc	360
caatgttgag	gcctgtggtt	atagtgatag	agtacaacaa	atcacactcg	ggaattcaac	420

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aataacaaca	caagaagcag	ccaacgctgt	tgtgtgttat	gctgaatggc	cagagtacct	480
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accagatgca	ctcaaggata	tgggtgtggt	cgggcaaaac	atgtttttcc	actcactagg	660
aagatcaggt	tacacagtac	a				681

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 <212> DNA
 <213> human Influenza A virus

<220>
 <223> primer no 12 multiplex assay

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<210> 140
 <211> 24
 <212> DNA
 <213> human Influenza A virus

<220>
 <223> primer no 13 multiplex assay

<400> 140
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<210> 141
 <211> 20
 <212> DNA
 <213> human Influenza B virus

<220>
 <223> primer no 14 multiplex assay

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<210> 142
 <211> 20
 <212> DNA
 <213> human Influenza B virus

<220>
 <223> primer no 15 multiplex assay

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<210> 143
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 <212> DNA
 <213> human Respiratory Syncytial Virus

<220>
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<210> 144
 <211> 23
 <212> DNA
 <213> human Respiratory Syncytial virus

<220>
 <223> primer no 17 multiplex assay

<400> 144
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48/52

<210> 145
 <211> 26
 <212> DNA
 <213> human Parainfluenza 1 virus

<220>
 <223> primer no 22 multiplex assay

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<210> 146
 <211> 26
 <212> DNA
 <213> human Parainfluenza 1 virus

<220>
 <223> primer no 23 multiplex assay

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<210> 147
 <211> 22
 <212> DNA
 <213> human Parainfluenza 1 virus

<220>
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 primer P1

<400> 147
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<210> 148
 <211> 22
 <212> DNA
 <213> human Parainfluenza 1 virus

<220>
 <223> human Parainfluenza 1 virus
 primer P2

<400> 148
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<210> 149
 <211> 26
 <212> DNA
 <213> human Parainfluenza 3 virus

<220>
 <223> primer no 24 multiplex assay

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<210> 150
 <211> 26
 <212> DNA
 <213> human Parainfluenza 3 virus

<220>
 <223> primer no 25 multiplex assay

<400> 150
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<210> 151
 <211> 25
 <212> DNA
 <213> human Parainfluenza virus

49/52

<220>
 <223> humna Parainfluenza virus
 primer P3

<400> 151
 tcttgcttca ttcttcaata caatc 25

<210> 152
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 <213> human Parainfluenza 3 virus

<220>
 <223> human Parainfluenza 3 virus
 primer P4

<400> 152
 aattccatca gagcttttaa tct 23

<210> 153
 <211> 18
 <212> DNA
 <213> human Adenovirus

<220>
 <223> primer human Adenovirus P5

<400> 153
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<210> 154
 <211> 26
 <212> DNA
 <213> human Adenovirus

<220>
 <223> primer no 26 multiplex assay

<400> 154
 cctacgcacg atgtgaccac agaccg 26

<210> 155
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 <212> DNA
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<220>
 <223> primer no 27 multiplex assay

<400> 155
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<210> 156
 <211> 21
 <212> DNA
 <213> human Sars Coronavirus

<220>
 <223> primer SARS no P5

<400> 156
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<210> 157
 <211> 21
 <212> DNA
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<220>
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 primer P6

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<400> 157
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 <210> 158
 <211> 24
 <212> DNA
 <213> human Sars Coronavirus
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 primer P7
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 <211> 22
 <212> DNA
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 <220>
 <223> human Sars Coronavirus
 primer P8
 <400> 159
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 <223> primer no 28 multiplex assay
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 <213> human Enterovirus/human Rhinovirus
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 <223> primer no 29 multiplex assay
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 <220>
 <223> probe no 30 multiplex assay
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 <213> human Influenza B virus
 <220>
 <223> probe no 31 multiplex assay
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<210> 164
 <211> 23
 <212> DNA
 <213> human Respiratory Syncytial virus

<220>
 <223> probe no 32 multiplex assay

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23

<210> 165
 <211> 23
 <212> DNA
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<220>
 <223> probe no 35 multiplex assay

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23

<210> 166
 <211> 23
 <212> DNA
 <213> human Parainfluenza 3 virus

<220>
 <223> probe no 36 multiplex assay

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23

<210> 167
 <211> 18
 <212> DNA
 <213> human Adenovirus

<220>
 <223> probe no 37 multiplex assay

<400> 167
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18

<210> 168
 <211> 23
 <212> DNA
 <213> human Rhinovirus

<220>
 <223> probe no 38 multiplex assay

<400> 168
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23

<210> 169
 <211> 23
 <212> DNA
 <213> human Enterovirus

<220>
 <223> probe no 39 multiplex assay

<400> 169
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23

<210> 170
 <211> 558
 <212> DNA
 <213> human Herpesvirus 2

<220>

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<223> modified human Herpesvirus 2
internal control
multiplex no 1

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<220>

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multiplex no 2

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<213> human Herpesvirus

<220>

<223> Internal Control probe no 42
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<400> 172

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